

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2005, 13:37:17 ; Search time 44 Seconds  
(without alignments)  
707.470 Million cell updates/sec

Title: US-10-081-280-6  
Perfect score: 2323  
Sequence: 1 MEQPRGCAAVAAALLVLL.....ERMGLDCGVEDLSRLQRP 417

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

## Listing first 45 summaries

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Database : Issued Patents AA:
1: /cgm2_6/ptodata/1/iaa/5A COMB pep.*
2: /cgm2_6/ptodata/1/iaa/5B COMB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2323	100.0	417	3	US-08-813-469-4	Sequence 4, Appli
2	2323	100.0	417	3	US-09-153-927-2	Sequence 2, Appli
3	2323	100.0	417	4	US-09-563-918-5	Sequence 5, Appli
4	2323	100.0	417	4	US-08-928-069-10	Sequence 10, Appli
5	2323	100.0	417	4	US-08-828-683A-6	Sequence 6, Appli
6	2323	100.0	417	4	US-09-557-908-4	Sequence 4, Appli
7	2323	100.0	417	4	US-09-874-138-5	Sequence 5, Appli
8	2323	100.0	417	4	US-09-333-966-4	Sequence 4, Appli
9	2323	100.0	446	4	US-09-949-016-7652	Sequence 7652, Ap
10	2323	100.0	833	3	US-09-013-895A-5	Sequence 5, Appli
11	2323	100.0	833	4	US-09-448-868-5	Sequence 5, Appli
12	2367	97.6	428	3	US-08-815-469-2	Sequence 2, Appli
13	2367	97.6	428	4	US-09-557-908-2	Sequence 2, Appli
14	2367	97.6	428	4	US-09-333-966-2	Sequence 2, Appli
15	1051	45.2	181	4	US-08-928-069-1	Sequence 1, Appli
16	1051	45.2	181	4	US-08-828-683A-1	Sequence 1, Appli
17	387.5	16.7	471	4	US-09-513-007-2	Sequence 2, Appli
18	376	16.2	455	1	US-08-050-319B-25	Sequence 25, Appli
19	376	16.2	455	2	US-08-463-982-25	Sequence 25, Appli
20	376	16.2	455	4	US-08-406-824A-4	Sequence 4, Appli
21	374.5	16.1	909	3	US-09-013-895A-4	Sequence 4, Appli
22	374.5	16.1	909	4	US-09-448-868-4	Sequence 4, Appli
23	374	16.1	455	1	US-08-321-668-2	Sequence 2, Appli
24	374	16.1	455	1	US-08-837-94-1	Sequence 2, Appli
25	374	16.1	455	2	US-08-126-016-2	Sequence 2, Appli
26	374	16.1	455	3	US-08-815-469-5	Sequence 5, Appli
27	374	16.1	455	3	US-09-006-353A-3	Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
 US-08-815-469-4  
 Sequence 4: Application US/08815469  
 Patent No. 6153402  
 GENERAL INFORMATION:  
 APPLICANT: Yu, Guo-Liang  
 APPLICANT: Ni, Jian  
 APPLICANT: Dixit, Vishva  
 APPLICANT: Gentz, Reiner L.  
 APPLICANT: Dillon, Patrick J.  
 TITLE OF INVENTION: Death Domain Containing Receptors  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
 STREET: 1100 New York Ave., NW, Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent-In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/815,469  
 FILING DATE: HEREWITH  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: No. 6153402 Yet Assigned  
 FILING DATE: 06-FEB-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/028,711  
 FILING DATE: 17-OCT-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/013,285  
 FILING DATE: 12-MAR-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Steffe, Eric K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 417 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

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US-08-815-469-4
Query Match      100.0%; Score 2323; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEQRPGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSAVADTRCGCKPG 120
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Qy 121 WFVECOVQSVSSPFYQPCDCLDGCALHRRHRLTLLCSRDDTCGCLPGFYEHGDCVSCP 180
Db 121 WFVECOVQSVSSPFYQPCDCLDGCALHRRHRLTLLCSRDDTCGCLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPHKPLVTAD EAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPHKPLVTAD EAG 240

Qy 241 MEALTPPPATHLSPLDSAHILLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHILLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300

Qy 301 DQPSRALGPAAPTLSPESPAGSPAMMLOPQPOLYDVMADVAPARRWKEFVRTTLGLREAE 360
Db 301 DQPSRALGPAAPTLSPESPAGSPAMMLOPQPOLYDVMADVAPARRWKEFVRTTLGLREAE 360

Qy 361 IEAVEVEIGRFDQOQYEMLKWRQOQAPAGLVAVVAALERMGLDGCVEDLRSRLQRP 417
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RESULT 3
US-09-565-918-5
; Sequence 5, Application US/09565918
; Patent No. 6433147
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/09/565,918
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-918-5

Query Match      100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEQRPGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSAVADTRCGCKPG 120

Qy 121 WFVECOVQSVSSPFYQPCDCLDGCALHRRHRLTLLCSRDDTCGCLPGFYEHGDCVSCP 180
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Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPHKPLVTAD EAG 240

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Db 241 MEALTPPPATHLSPLDSAHILLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300

Qy 301 DQPSRALGPAAPTLSPESPAGSPAMMLOPQPOLYDVMADVAPARRWKEFVRTTLGLREAE 360
Db 301 DQPSRALGPAAPTLSPESPAGSPAMMLOPQPOLYDVMADVAPARRWKEFVRTTLGLREAE 360

Qy 361 IEAVEVEIGRFDQOQYEMLKWRQOQAPAGLVAVVAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFDQOQYEMLKWRQOQAPAGLVAVVAALERMGLDGCVEDLRSRLQRP 417

RESULT 2
US-09-153-927-2
; Sequence 2, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDonnell, Peter C.
; APPLICANT: Young, Peter R.
; APPLICANT: Zou, Jun
; TITLE OF INVENTION: A Method of Identifying Agonists and
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; TITLE OF INVENTION: and TR5
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153,927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061,334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Human
US-09-153-927-2

Query Match      100.0%; Score 2323; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEQRPGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

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Qy 121 WFVECOVQSVSSPFYQPCDCLDGCALHRRHRLTLLCSRDDTCGCLPGFYEHGDCVSCP 180
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QY 361 IEAVEVEIGRFDQOQYEMLKRWROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGP 417  
DB 361 IEAVEVEIGRFDQOQYEMLKRWROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGP 417

## RESULT 4

US-08-928-069-10  
; Sequence 10, Application US/08928069  
; Patent No. 6462176  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,069  
; FILING DATE: 11-Sep-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/026943  
; FILING DATE: 09/23/1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P105281  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-928-069-10

Query Match 100.0%; Score 2323; DB 4; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.1e-193;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEQPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
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DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCPHPKPLVTADEAG 240  
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QY 361 IEAVEVEIGRFDQOQYEMLKRWROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGP 417  
DB 361 IEAVEVEIGRFDQOQYEMLKRWROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGP 417

## RESULT 5

US-08-828-683A-6  
; Sequence 6, Application US/08828683A  
; Patent No. 6469144  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,683A  
; FILING DATE: 31-Mar-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/625328  
; FILING DATE: 1-Apr-1996  
; APPLICATION NUMBER: 08/710802  
; FILING DATE: 23-Sep-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1007P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-08-828-683A-6

Query Match 100.0%; Score 2323; DB 4; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.1e-193;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEQPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
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QY 121 WFVEQVQSQVSSSPFYCQPCLDGALHRRHRLTLCSRRDTCGTCPLPGFYEHGDCVSCP 180  
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QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCPHPKPLVTADEAG 240  
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCPHPKPLVTADEAG 240

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DB 241 MEALTPPPATHSLPDSAHLLAPPDSSEKICTVOLVGNSTWTPGYPETOALCPQVTSW 300  
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DB 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360  
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DB 361 IEAVEVEIGRFRDOOYEMLKRWRQOOPAGLGAHVAAALERMGLDGCVEDLRSRLQGRP 417  
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RESULT 6  
US-09-557-908-4  
; Sequence 4, Application US/09557908  
; Patent No. 6713061  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; FILE REFERENCE: 1488.0310008  
; CURRENT APPLICATION NUMBER: US/09/557,908  
; CURRENT FILING DATE: 2000-04-21  
; PRIOR APPLICATION NUMBER: US 60/136,741  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 60/130,488  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 08/815,469  
; PRIOR FILING DATE: 1997-03-11  
; PRIOR APPLICATION NUMBER: US 60/037,341  
; PRIOR FILING DATE: 1997-02-06  
; PRIOR APPLICATION NUMBER: US 60/028,711  
; PRIOR FILING DATE: 1996-10-17  
; PRIOR APPLICATION NUMBER: US 60/013,285  
; PRIOR FILING DATE: 1996-03-12  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-557-908-4

Query Match 100.0%; Score 2323; DB 4; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.1e-193;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MEQPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
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QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
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DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
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QY 121 WFVECVQSQVSSSPFFYQPCCLDCGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180  
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RESULT 7  
US-09-874-138-5  
; Sequence 5, Application US/09874138  
; Patent No. 6743625  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Death Domain Containing Receptor 5  
; FILE REFERENCE: 1488.1310006  
; CURRENT APPLICATION NUMBER: US/09/874,138  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/565,009  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/148,939  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: 60/133,238  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/132,498  
; PRIOR FILING DATE: 1999-05-04  
; PRIOR APPLICATION NUMBER: 09/042,583  
; PRIOR FILING DATE: 1998-03-17  
; PRIOR APPLICATION NUMBER: 60/054,021  
; PRIOR FILING DATE: 1997-07-29  
; PRIOR APPLICATION NUMBER: 60/040,846  
; PRIOR FILING DATE: 1997-03-17  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-874-138-5

Query Match 100.0%; Score 2323; DB 4; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.1e-193;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEQPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
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DB 1 MEQPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
|||||  
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
|||||  
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
|||||  
QY 121 WFVECVQSQVSSSPFFYQPCCLDCGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180  
|||||  
DB 121 WFVECVQSQVSSSPFFYQPCCLDCGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180  
|||||  
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGNLTLYTYRHCHWPHKPLVTAD EAG 240  
|||||  
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGNLTLYTYRHCHWPHKPLVTAD EAG 240  
|||||  
QY 241 MEALTPPPATHSLPDSAHLLAPPDSSEKICTVOLVGNSTWTPGYPETOALCPQVTSW 300  
|||||  
DB 241 MEALTPPPATHSLPDSAHLLAPPDSSEKICTVOLVGNSTWTPGYPETOALCPQVTSW 300  
|||||  
QY 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360  
|||||  
DB 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360  
|||||  
QY 361 IEAVEVEIGRFRDOOYEMLKRWRQOOPAGLGAHVAAALERMGLDGCVEDLRSRLQGRP 417  
|||||



Db 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAIVAAALERMGLDGCVEDLRSRLQRP 417

RESULT 8  
US-09-333-966-4  
; Sequence 4, Application US/09333966  
; Patent No. 6759513  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/333,966  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,469  
; FILING DATE:  
; APPLICATION NUMBER: 6759513 Yet Assigned  
; FILING DATE: 06-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/028,711  
; FILING DATE: 17-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,285  
; FILING DATE: 12-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-333-966-4

Query Match 100.0%; Score 2323; DB 4; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.1e-193;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Db 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120

QY 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180  
Db 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180

QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADGAG 240  
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADGAG 240

QY 241 MEALTTPPATHLSPLDLSAHTLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300  
Db 241 MEALTTPPATHLSPLDLSAHTLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300

QY 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLLGLRAE 360  
Db 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLLGLRAE 360

QY 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAIVAAALERMGLDGCVEDLRSRLQRP 417  
Db 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAIVAAALERMGLDGCVEDLRSRLQRP 417

RESULT 9  
US-09-949-016-7652  
; Sequence 7652, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7652  
; LENGTH: 446  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7652

Query Match 100.0%; Score 2323; DB 4; Length 446;  
Best Local Similarity 100.0%; Pred. No. 1.2e-193;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Db 30 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 89

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120  
Db 90 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 149

QY 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180  
Db 150 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 209

QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADGAG 240  
Db 210 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADGAG 269

QY 241 MEALTTPPATHLSPLDLSAHTLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300  
Db 270 MEALTTPPATHLSPLDLSAHTLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 329

QY 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLLGLRAE 360  
Db 330 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLLGLRAE 389

QY 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAIVAAALERMGLDGCVEDLRSRLQRP 417  
Db 390 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAIVAAALERMGLDGCVEDLRSRLQRP 446

```
RESULT 10
US-09-013-895A-5
; Sequence 5, Application US/09013895A
; Patent No. 6342363
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013.895A
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-013-895A-5

Query Match 100.0%; Score 2323; DB 3; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.7e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCQDPTFLAWNHNSCARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCQDPTFLAWNHNSCARCOACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVECVQSQVSSSPFFYQPCPLDCGALHRRHLLCSRRDTCGTLPGFYEHGDCVSCP 180
Db 121 WFVECVQSQVSSSPFFYQPCPLDCGALHRRHLLCSRRDTCGTLPGFYEHGDCVSCP 180
QY 181 TSTLGSCPERCAAVCGWQMFVQVLLAGLVVPLLGLATLYTYRHCHPPLVTADEAG 240
Db 181 TSTLGSCPERCAAVCGWQMFVQVLLAGLVVPLLGLATLYTYRHCHPPLVTADEAG 240
QY 241 MEALTPTPPATHLSPLDSSAHTLLAPDSSEKICTVOLVGNWSTPGYPETOALCPQVTSW 300
Db 241 MEALTPTPPATHLSPLDSSAHTLLAPDSSEKICTVOLVGNWSTPGYPETOALCPQVTSW 300
QY 301 DOLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTILGLREAE 360
Db 301 DOLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTILGLREAE 360

RESULT 11
US-09-448-868-5
; Sequence 5, Application US/09448868
; Patent No. 6461823
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448.868
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-448-868-5

Query Match 100.0%; Score 2323; DB 4; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.7e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCQDPTFLAWNHNSCARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCQDPTFLAWNHNSCARCOACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVECVQSQVSSSPFFYQPCPLDCGALHRRHLLCSRRDTCGTLPGFYEHGDCVSCP 180
Db 121 WFVECVQSQVSSSPFFYQPCPLDCGALHRRHLLCSRRDTCGTLPGFYEHGDCVSCP 180
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Qy	181	TSTL	SGCP	RC	AA	VC	GM	FW	VQ	VL	LAG	V	VP	LL	L	GAT	LT	TY	TR	HC	WH	PK	PL	VT	DA	EA	G	240																										
Db	181	TSTL	SGCP	RC	AA	VC	GM	FW	VQ	VL	LAG	V	VP	LL	L	GAT	LT	TY	TR	HC	WH	PK	PL	VT	DA	EA	G	240																										
Qy	241	MEAL	TP	PP	ATH	LS	PL	DS	AA	HT	LL	AP	DS	SE	K	I	CT	VT	Q	N	S	WT	PG	Y	P	ET	Q	EA	LC	PQ	VT	WS	300																					
Db	241	MEAL	TP	PP	ATH	LS	PL	DS	AA	HT	LL	AP	DS	SE	K	I	CT	VT	Q	N	S	WT	PG	Y	P	ET	Q	EA	LC	PQ	VT	WS	300																					
Qy	301	DQ	L	P	RA	L	G	P	AA	A	PT	L	S	P	E	S	P	A	G	S	P	A	M	L	O	P	G	P	O	L	Y	D	V	M	D	A	V	P	A	R	R	K	E	F	V	R	T	L	G	L	E	A	E	360
Db	301	DQ	L	P	RA	L	G	P	AA	A	PT	L	S	P	E	S	P	A	G	S	P	A	M	L	O	P	G	P	O	L	Y	D	V	M	D	A	V	P	A	R	R	K	E	F	V	R	T	L	G	L	E	A	E	360
Qy	361	I	E	A	V	E	I	G	R	F	R	D	O	O	Y	E	M	L	K	R	W	O	O	P	A	G	L	G	A	N	V	A	A	L	R	M	G	L	D	C	G	V	E	D	L	R	S	L	O	R	P	417		
Db	361	I	E	A	V	E	I	G	R	F	R	D	O	O	Y	E	M	L	K	R	W	O	O	P	A	G	L	G	A	N	V	A	A	L	R	M	G	L	D	C	G	V	E	D	L	R	S	L	O	R	P	417		

RESULT 12  
US-08-815-469-2  
; Sequence 2, Application US/08815469  
; Patent No. 6153402  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Steirne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600

Query Match 97.6%; Score 2267; DB 3; Length 428;  
Best Local Similarity 97.1%; Pred.No. 8.6e-189;  
Matches 409; Conservative 1; Mismatches 5; Indels

[illegible]

QY 3 QRPRG-----CAAVAAALLVLLGARAQGGTRSPRCDGDFHKKIGLFCRCRCPAGHY 56



CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/026943  
FILING DATE: 09/23/1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Marchang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1052R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 181 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-928-069-1

Query Match 45.2%; Score 1051; DB 4; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1.3e-83;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEQRPRGCAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60  
Db 1 MEQRPRGCAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60  
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSSAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSSAVADTRCGCKPG 120  
Qy 121 WFVECVSQCVSSSPFYQPCPLDCGALHRTLLCSRRDTCGTCLPGFYEHGDCVSCP 180  
Db 121 WFVECVSQCVSSSPFYQPCPLDCGALHRTLLCSRRDTCGTCLPGFYEHGDCVSCP 180  
Qy 181 T 181  
Db 181 T 181

Search completed: June 27, 2005, 13:44:23  
Job time : 46 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2005, 13:37:13 ; Search time 19 Seconds  
(without alignments)  
2111.705 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323  
Sequence: 1 MEQPRGCAVAAALLVLL.....ERMGLDGCVEDLRSLQRP 417

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	415	17.9	461	2 JC4302	tumor necrosis fac
2	404.5	17.4	454	1 GOMST1	tumor necrosis fac
3	394.5	17.0	461	1 GORTT1	tumor necrosis fac
4	374	16.1	455	1 GORTU1	tumor necrosis fac
5	199.5	8.6	335	2 A40036	apoptosis-mediati
6	196	8.4	327	2 A46484	apoptosis-mediati
7	175	7.5	324	2 JC2395	Fas antigen precu
8	168	7.2	314	2 I37383	FAS soluble protei
9	166	7.1	435	2 I54182	tumor necrosis fac
10	163.5	7.0	1548	2 S34583	serine proteinase
11	162.5	7.0	349	2 D36858	gene G4R protein -
12	159.5	6.9	348	2 T28623	hypothetical prote
13	158	6.8	425	1 A36431	nerve growth facto
14	158	6.8	1574	2 T13954	MEGF6 protein - ra
15	155.5	6.7	427	1 GQHUN	nerve growth facto
16	154.5	6.7	349	2 D21715	G2R protein - vari
17	153.5	6.6	272	2 I48700	gene ox40 protein
18	153.5	6.6	651	2 JC7705	death receptor-6 -
19	153.5	6.6	915	1 A48225	subtilisin-like pr
20	149.5	6.4	3707	2 S18252	heparan sulfate pr
21	148	6.4	2823	2 F87908	protein T22A3.8 li
22	148	6.4	2823	2 T23064	hypothetical prote
23	148	6.4	3102	2 T43291	laminin alpha chai
24	147.5	6.3	1801	1 MMRTS	laminin beta-2 cha
25	146.5	6.3	2531	2 T31070	notch homolog - se
26	146	6.3	277	2 A60771	B-cell activation
27	146	6.3	667	2 A48579	trophozoite surfac
28	145.5	6.3	416	1 JN0006	nerve growth facto
29	145	6.2	3635	2 T10053	laminin alpha 5 ch

30 144.5 6.2 326 1 GOVZML T2 protein - myxom  
31 144.5 6.2 1680 2 A43434 furin (EC 3.4.21.7  
32 143.5 6.2 915 2 B48225 probable proteol  
33 143.5 6.2 4391 2 A38096 perlecan precursor  
34 142 6.1 1557 2 T28811 hypothetical prote  
35 141.5 6.1 686 2 JC7569 Delta-4 protein -  
36 138.5 6.0 1299 2 T43251 furin (EC 3.4.21.7  
37 138 5.9 271 2 S12783 OX40 antigen precu  
38 138 5.9 305 2 A46476 B cell-associated  
39 138 5.9 1607 1 MMMSB2 laminin gamma-1 ch  
40 138 5.9 1609 1 MMHUR2 laminin gamma-1 ch  
41 137.5 5.9 642 1 S52111 uromodulin precu  
42 137.5 5.9 1798 2 S53869 laminin beta-2 cha  
43 136.5 5.9 260 1 A46517 CD27 antigen precu  
44 136.5 5.9 2219 2 T27684 hypothetical prote  
45 136.5 5.9 3712 2 S18253 laminin alpha-1 ch

ALIGNMENTS

RESULT 1

JC4302 tumor necrosis factor receptor p55 precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004

C:Accession: JC4302; PC4093

R:Suter, B.; Pauli, U.

Gene 163, 263-266, 1995

A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

A:Reference number: JC4302; MUID:96011645; PMID:7590278

A:Accession: JC4302

A:Molecule type: mRNA

A:Residues: 1-461 <SUT>

A:Cross-references: UNIPROT:P50555; GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g114175

A:Accession: PC4093

A:Molecule type: protein

A:Residues: 1-7 <SU2>

A:Experimental source: kidney cell line 15

C:Genetics:

A:Gene: tnfr

C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog

C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>

F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>

F:44-82/Domain: NGF receptor repeat homology <NGI>

F:84-126/Domain: NGF receptor repeat homology <NGF>

F:211-231/Domain: transmembrane #status predicted <TMM>

F:7361-447/Domain: signal transduction #status predicted <SIT>

F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.9%; Score 415; DB 2; Length 461;

Best Local Similarity 30.5%; Pred. No. 1.5e-20;

Matches 140; Conservative 44; Mismatches 201; Indels 74; Gaps 18;

QY 11 VAAALLVLLGARAQG-----GTRSPR---CDCAGDFHKIGLFCRCGCPAGHYLKAPT 62

Db 14 VLRAALLVDVYPAGVHGLVHPGDRKRESLCPQGYKSHPNRSICCTCKHGKTYLHNDCL 73

QY 63 BPCGNSTCLVCPQDTFLAWHNHNSCARQACDAQSQAVALNCNSAVADTRCGCKPGWF 122

Db 74 GPGLDTRCREDNQFTTASEN-HLTQCLSCSKRSEMSQVSEISPTVDRTVCGCRKN-- 130

QY 123 VECQVSQCVSSSPFCQPCLDGALHRRHTRLLC-SRRDTCGTCLPGPYEHGDCGVSCPT 181

Db 131 ---QTRKWTSTLFOCLNCSLCP--NGTVQPLCKLEKQDTIC-NHSGFFLDKCEVCSCVN 184

QY 182 STLGSCEPCERCAAVCGWRQMF-----WVQVLLAGLVVPLLLGATLTYYTHCWPH--- 230

Db 185 CKNADCKNLCPATSETRNDFODTGTGTVLLPLVIFPGLCLAFFLVGLACRYQWRKPKLYS 244

QY 231 -----KPLVTADAGMEALTPPPATHLSPLD--SAHTLLAPDSSSEKICTV 274



Db 245 IICGKSTPVKGEPEPLATAPSG-----PIITFSPISPSPTTTPSPVPSFPISSP 297  
QY 275 QLVGNSWT---PGVPETQEQALCPQVTSWDQLPSRALGPAAPATLSP-----ESPAG 323  
Db 298 TFTPDCWNSNIKVTSPKKEIAPPPQAG-----PILMPMPASTPVTPLPKWGGSAHSAHS 352  
QY 324 SPAMMLQGPQ-QLYDVMDAVARRKKEFVRTLGLEAREIEAVEVEIGR-FRDQOVEMLKR 381  
Db 353 APAQLADADPATLYAVDGVPTTRKKEFVRRLGLSEHIELELQNGCLREAOYSLMAE 412  
QY 382 WRQ-----QQPAGLGVYAALERMGLDGCVEDLSRLQRP 417  
Db 413 WRRRTSRREATLELLGSLVRDMDLLGCLDIEEAL-RGP 450  
RESULT 2  
QOMST1  
tumor necrosis factor receptor 1 precursor - mouse  
N:Alternate names: tumor necrosis factor receptor, 55K  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: A38634; B40254; S16677; S19021; I54532; I57826  
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.  
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r  
A:Reference number: A38634; MUID:91187885; PMID:1849278  
A:Accession: A38634  
A:Molecule type: mRNA  
A:Residues: 1-454 <LEW>  
A:Cross-references: UNIPROT:P25118; GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826  
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
A:Reference number: A40254; MUID:91246168; PMID:1645445  
A:Accession: B40254  
A:Molecule type: mRNA  
A:Residues: 1-454 <GO>  
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826  
R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Feldma  
Eur. J. Immunol. 21, 1649-1656, 1991  
A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis  
A:Reference number: S16677; MUID:91285014; PMID:1647956  
A:Accession: S16677  
A:Molecule type: mRNA  
A:Residues: 1-454 <BAR>  
A:Cross-references: EMBL:X59238; NID:G53578; PIDN:CAA41922.1; PID:G53579  
R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.  
Immunogenetics 34, 338-340, 1991  
A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.  
A:Reference number: S19021; MUID:92039815; PMID:1657766  
A:Accession: S19021  
A:Molecule type: mRNA  
A:Residues: 1-454 <ROT>  
A:Cross-references: EMBL:X57796; NID:G54848; PIDN:CAA40936.1; PID:G54849  
R:Bebo, B.F.  
Immunogenetics 39, 450-451, 1994  
A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1  
A:Reference number: I54532; MUID:94245292; PMID:8188324  
A:Accession: I54532  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-454 <RES>  
A:Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733  
R:Rothe, J.G.; Bluthmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.  
Mol. Immunol. 30, 165-176, 1993  
A:Title: Genomic organization and promoter function of the murine tumor necrosis factor  
A:Reference number: I57826; MUID:93156721; PMID:8381516  
A:Accession: I57826  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-393, 'G', 395-454 <RE2>  
A:Cross-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102

C:Comment: This protein is one of two distantly related receptors for both TNF-alpha (cac  
C:Genetics:  
A:Gene: TNFR-2  
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog  
C:Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
F:30-212/Domain: extracellular #status predicted <EXT>  
F:44-82/Domain: NGF receptor repeat homology <NG1>  
F:84-126/Domain: NGF receptor repeat homology <NG2>  
F:127-167/Domain: NGF receptor repeat homology <NG3>  
F:168-204/Domain: NGF receptor repeat homology <NG4>  
F:213-235/Domain: transmembrane #status predicted <MEM>  
F:236-454/Domain: intracellular #status predicted <INT>  
F:54,151,202/Binding site: carboxylate (Asn) (covalent) #status predicted  
Query Match 17.4%; Score 404.5; DB 1; Length 454;  
Best Local Similarity 27.2%; Pred. No. 7.5e-20;  
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 18;  
QY 11 VAALLLVILGARQGGT-----RSPRCDCAGDPHKKILGLFCCRCPCPAGHYLKA 59  
Db 11 LSLVLLALLMGIHPSGVTGLVPSLGDREKDSLCPQGYVHSKNSICCTCKCHKGTLYVS 70  
QY 60 PCTEPCGNSTCLVCPQDTFLAWENHNHSECAQCAQCEQASQVALENCSAVADTRCGCKP 119  
Db 71 DCPSFGDRTVCRECEKGTFTASQNYLR-QCLSCYCKREMSQVEISPCQADKDTVCCK- 128  
QY 120 GWFVECVQSVSSPPYCPCLDCGALHRHRLLCRRDTCCTCLPGFVEHGDGVCVC 179  
Db 129 ----ENQFQVLSETHFQVDCSPC---FNGVTVPCKETQNTQVNCNCHAGFFLRESECVPC 182  
QY 180 PTSTLGGSCP--ERCAAVC-----GWQMFVQVVLGLAVVPLLGLATLFTY 224  
Db 183 ----SHCKKNEECMKLCLPPLANVTPQDSGTAVALLLPLVLLGLCLLSFIFSLMCRY 237  
QY 225 RHQWP-----HKPLVTADEAGMEALTPPAPATHLSPLDSAHTLL-----APDSEK 270  
Db 238 PRWRPEVYSIICRDPVPVKEKAGKPLTPAPSPAFSTSGFNPTLGFSTPGFSSVSTP 297  
QY 271 ICTVOLVGNW-----TPGY-PETQEQALC----POVTSWDQLPSRALGPAAP 314  
Db 298 ISPI-FGFSNNHFMPPVSEVVPTQGADPLLYESLCSVPAPTSVQKWD----- 344  
QY 315 TLPSPESAGSPAMMLQGPOLYDMDAVPARRKKEFVRTLGLEAREIEAVEVEIGR-FRD 373  
Db 345 SAHPQRPDNDALAI-----LYAVDGVPPARWKKEFMRFMGLSEHERLEMQNGRCURE 398  
QY 374 QQYEMLKRWQQQPA---GLGAVYAALERMGLDGCVEDLSRLQRP 417  
Db 399 AQYSMLEAWRRRTPRHEDTLEVVGLVLSKKNLACLENILEAL-RNP 444  
RESULT 3  
QORTT1  
N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Jun-1992 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: B36555  
R:Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; (C  
DNA Cell Biol. 9, 705-715, 1990  
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor  
A:Reference number: A36555; MUID:91090841; PMID:1702293  
A:Accession: B36555  
A:Molecule type: mRNA  
A:Residues: 1-461 <HIM>  
A:Cross-references: UNIPROT:P22934; GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362  
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <SIG>



A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A:Reference number: A35010; MUID:90110215; PMID:2153136  
A:Accession: A35010  
A:Molecule type: protein  
A:Residues: 41-45 <ENG>  
A:Experimental source: normal urine  
F:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994  
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f  
A:Reference number: JC2404; MUID:95128033; PMID:7765720  
A:Accession: JC2404  
A:Molecule type: protein  
A:Residues: 41-53, 'X', '55-144, 'X', '146-150, 'X', '152-186, 'X', '188-201 <KAJ>  
A:Experimental source: urine  
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
C:Genetics:  
A:Gene: GDB:TNFR1  
A:Cross-references: GDB:125913; OMIM:191190  
A:Map position: 12p13.2-12p13.2  
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <SIG>  
F:30-211/Domain: extracellular #status predicted <EXT>  
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
F:44-82/Domain: NGF receptor repeat homology <NG1>  
F:84-126/Domain: NGF receptor repeat homology <NG2>  
F:127-167/Domain: NGF receptor repeat homology <NG3>  
F:168-196/Domain: NGF receptor repeat homology <NG4>  
F:212-234/Domain: transmembrane #status predicted <INT>  
F:235-455/Domain: intracellular #status predicted <MEM>  
F:54, 145, 151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.1%; Score 374; DB 1; Length 455;  
Best Local Similarity 28.3%; Pred. No. 8.2e-18;  
Matches 131; Conservative 49; Mismatches 183; Indels 100; Gaps 22;  
  
Qy 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63  
Db 15 LLELVGLYPSGVGLVPHLDREKRSVCPQGYKIHPPNNISICTCKHGYILYNDPCG 74  
  
Qy 64 PCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVADTRCGCKPGWFFV 123  
Db 75 PGQDTRCECSGSFTASENHLR-HCLSCSKCKEMGQVEISSCTVDRDITVCGCKNQYR 133  
  
Qy 124 EC---QVSSQVSSSPFFYQPCDCLDGHRLHRLTLCSRRDTCGCLPGFYEHGDCVSCP 180  
Db 134 HWYSENLFQC-----FNCSLCLN-GTVH---LSCQEKQNTVCTCHAGFFLRENECVSC- 182  
  
Qy 181 TSLTSGCPE--RCAAVC-----GWQMFVQVLLAGLVVPLLLGATILTYTYRH 226  
Db 183 ----SNCKSLKCTKCLPQENVKGTEDSGTIVLLPLVIFPGLCLSLFGLMYRYQR 238  
  
Qy 227 CWPHK-----PLVTADEAGMEALTPPPATHLSPDLS-----AHTLAPDPSSEKIC 272  
Db 239 -WKSPLYIVCKSTPEKEGELEGTTPK---LAPNFSFPTPGTPTLGLSPVPSSTFT 294  
  
Qy 273 TVQLVGNWSWTPGYETQALCPQVTSWDQLPSRALGP-----AAAPTLS- 318  
Db 295 S-----SSTYTFGD-----CFNFA-----APREVAAPPYQAGDPIALALASDPIPNPL 338  
  
Qy 319 ---ESPAGSPAMMLQPGP-QLYDVMDAVPARRWKEFVRTLLGLREAEIEAVEVEIGR-FRD 373  
Db 339 QKWDSAHKPOSLODDPATLYAVVENVPLRWKEFVRLGLSDHEIDRLQLQGRCLURE 398  
  
Qy 374 QQYEMLKWRQQQP---AGLGAVYAALERMGLDGCVEDLRSRL 413  
Db 399 AQYSMLATWRRRTTFRREATLELLGRVLRMDMLLGCLDEIEAL 441

RESULT 5  
A40036

apoptosis-mediating surface antigen Fas precursor - human  
N:Alternate names: surface antigen APO-1  
C:Species: Homo sapiens (man)  
C:Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 09-Jul-2004  
C:Accession: A40036; S24543; A38142  
F:Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase, H.  
Cell 66, 233-243, 1991  
A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediat  
A:Reference number: A40036; MUID:91309137; PMID:1713127  
A:Accession: A40036  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-335 <ITO>  
A:Cross-references: UNIPROT:P25445; GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410  
R:Krammer, P.H.  
submitted to the EMBL Data Library, February 1992  
A:Reference number: S24543  
A:Accession: S24543  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-335 <KRA>  
A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742  
F:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Richter  
J. Biol. Chem. 267, 10709-10715, 1992  
A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member c  
A:Reference number: A38142; MUID:92268122; PMID:1375228  
A:Accession: A38142  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-134, 'Q', '136-335 <OEH>  
A:Experimental source: SKW6.4 cells  
A:Note: sequence extracted from NCBI backbone (NCBIP:103810)  
A:Note: in NCBI backbone the source is designated as mouse  
C:Genetics:  
A:Gene: GDB:APF1  
A:Cross-references: GDB:132671; OMIM:134637  
A:Map position: 10q24.1-10q24.1  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog  
C:Keywords: apoptosis; surface antigen; transmembrane protein  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:85-128/Domain: NGF receptor repeat homology <NG4>  
F:174-190/Domain: transmembrane #status predicted <TMM>  
  
Query Match 8.6%; Score 199.5; DB 2; Length 335;  
Best Local Similarity 21.4%; Pred. No. 2.8e-06;  
Matches 74; Conservative 43; Mismatches 106; Indels 123; Gaps 12;  
  
Qy 44 GLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVA 103  
Db 56 GQFCHKPCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRRCLCDEGHGLEV 115  
  
Qy 104 LENCASVADTRCGCKPGWFFVEQVSCVSSSPFFYQPCDCLDGHRLHRLTLCSRRDTCG 163  
Db 116 EINCTQNTQKCRCKPNFF-----CNSTVCEHCDPCTKC----- 149  
  
Qy 164 TCLPGFYEHGDCGVCSTLTGSCPERCAAVCGWR-OMFWVOVLLAGLVVPLLLGATLTY 222  
Db 150 -----EHGI-IKECYLTSTNCKEB-----GSRNLGWLCLLL--LPIPLIIVWVKE 194  
  
Qy 223 TYRHCWPHKPLVTADAEAGMEALTPPPATHLSPDLSAHTL---LAPDPSSEKICTVQLVGN 279  
Db 195 VQKTCRKHR---KENQG-----SHESPTLNPTVAINTLSDVLSKYITTI----- 236  
  
Qy 280 SWTPGYETQALCPQVTSWDQLPSRALGPAAAPTLSPPSPAGSPAMMLQPGQLVDVM 339  
Db 237 -----AGVMTLS----- 243  
  
Qy 340 DAVPARRWKEFVRTLLGLREAEIEAVEVE-IGRFRDQQYEMLKWRQ 384  
Db 244 -----QVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRWHQ 283

RESULT 6

A46484  
apoptosis-mediating membrane-associated polypeptide Fas - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A46484; A47254  
R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, J. Immunol. 148, 1274-1279, 1992  
A:Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas and Fas ligand genes  
A:Reference number: A46484; MUID:92148151; PMID:1371136  
A:Accession: A46484  
A:Molecule type: mRNA  
A:Status: preliminary  
A:Residues: 1-327 <WAT>  
A:Cross-references: UNIPROT:P25446; GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226  
A:Experimental source: BAW3 macrophage cell line  
A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)  
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.  
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
A:Title: Aberrant transcription caused by the insertion of an early transposable element  
A:Reference number: A47254; MUID:93189576; PMID:7680478  
A:Accession: A47254  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-96 <ADA>  
A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506  
A:Experimental source: MRL lpr/lpr  
A:Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126863, NCBIN:126864)  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog  
C:Keywords: transmembrane protein  
F:44-79/Domain: NGF receptor repeat homology <NGF>  
F:81-124/Domain: NGF receptor repeat homology <NG4>  
F:181-124/Domain: NGF receptor repeat homology <NG4>

Query Match 8.4%; Score 196; DB 2; Length 327;  
Best Local Similarity 23.8%; Pred. No. 4.7e-06;  
Matches 62; Conservative 25; Mismatches 109; Indels 64; Gaps 8;

Qy 13 AALLVILGARAQGGTRSPRC-----DCAGDFHKKIGLFCRCGCPAGHY 56  
Db 6 AVLPLVLVLGALPVLNVRMQGTDSTFEGLELKRVRVETDNNCSGLY-QVGPFCCQCPQG 64  
Qy 57 LKAPCTPCGNSCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCASAVADTRC 116  
Db 65 KVEDCKWNGGTPCAPCTEGKEYMDKNHYADKCRCTLCDDEHGLEVEVETNCTQTNTK 124  
Qy 117 CKPGHVEFCQVSSQVSSFFPYCQPCDCLGALHRRHRLLCSSRDTRDTCGCLPFGVEHGDGC 176  
Db 125 CKP-----DFYCDSE-----EG-CEHCVRVC 142  
Qy 177 VSCPTSTLGCSPERCAAVC---GWRQMFVQVLLAGLVVPLLLGATLTYTYRHCHWPKPL 233  
Db 143 ASCERHGLEPCTATNTNCRKQSPRNRLWLLTLV-LLIPLVF-IYRKYRKRCWKRRQD 200  
Qy 234 VTADGMEALTPPPATHLS 253  
Db 201 DPESRTSSRETIPTMNASNLS 220

RESULT 7  
JC2395  
Fas antigen precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: JC2395; PC2246  
R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.  
Biochem. Biophys. Res. Commun. 198, 666-674, 1994  
A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver  
A:Reference number: JC2395; MUID:94128114; PMID:7507668  
A:Accession: JC2395  
A:Molecule type: mRNA  
A:Residues: 1-324 <KIM>  
A:Cross-references: UNIPROT:Q63199; DBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:dl005  
A:Experimental source: thymus  
A:Accession: PC2246

A:Molecule type: mRNA  
A:Residues: 1-62, 'RFT' <XI2>  
A:Cross-references: DBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:dl005651; PID:g468489  
A:Experimental source: liver  
C:Genetics:  
A:Introns: 62/1  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog  
C:Keywords: transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-324/Product: Fas antigen #status predicted <MAT>  
F:44-79/Domain: NGF receptor repeat homology <NGF>  
F:81-124/Domain: NGF receptor repeat homology <NG4>  
F:171-188/Domain: transmembrane #status predicted <TMM>

Query Match 7.5%; Score 175; DB 2; Length 324;  
Best Local Similarity 28.5%; Pred. No. 0.00012;  
Matches 43; Conservative 17; Mismatches 67; Indels 24; Gaps 5;

Qy 11 VARALLVLVG---ARAQG-----GTRSPRCDGAGDFHKKIGLFCRCGCPAG 54  
Db 4 IMAVLPLVLGALPVLNVRMQGTDSTFEGLELKRVRVETDNNCSGLY-QVGPFCCQCPQG 62  
Qy 55 HYLKAPCTPCGNSCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCASAVADTR 114  
Db 63 ERKYKDCITTSAGATCTCHPCTEGEYTDKHYSDKRCRCAFCDEGHGLEVEVETNCTQTNTK 122  
Qy 115 CGCKPGHVEFCQVSSQVSSFFPYCQPCDCLDGC 145  
Db 123 CRCKENFY--CNASLIC-----DHCVHCTSCG 146

RESULT 8  
I37383  
FAS soluble protein - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Jul-1995 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I37383  
R:Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.  
J. Immunol. 154, 2706-2713, 1995  
A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are  
A:Reference number: I37383; MUID:95181785; PMID:7533181  
A:Accession: I37383  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-314 <RES>  
A:Cross-references: UNIPROT:P25445; EMBL:Z47993; NID:g728578; PIDN:CAA88031.1; PID:g69555;  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog

Query Match 7.2%; Score 168; DB 2; Length 314;  
Best Local Similarity 19.1%; Pred. No. 0.00034;  
Matches 66; Conservative 37; Mismatches 100; Indels 142; Gaps 10;

Qy 44 GLFCRCGPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNHNSCARQACDEQASQVA 103  
Db 56 GQFCHKPCPGERKARDCTVNGDEPDCVPCQEGEYTDKAHPSKRCRCLCDEGHGLEV 115  
Qy 104 LENCASAVADTRCGCKPGHVEFCQVSSQVSSFFPYCQPCDCLGALHRRHRLLCSSRDTRDGC 163  
Db 116 EINCTRTQNTKCRCKPNFF-----CNSTVCEHCDPCTKC----- 149  
Qy 164 TCLPFGVEHGDGCVSPTSTLGCSPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYT 223  
Db 150 -----EHGI-IKECTLTSTNCKEE-----VKRKEV 174  
Qy 224 YRHCHPHKPLVTADGMEALTPPPATHLSPLDSAHTL---LAPDSSEKICTVOLVGN 280  
Db 175 QKTRKHR-----KENQG-----SHESTLPETVAINLSVDLSKYITTI----- 215  
Qy 281 WTPGYPTEQALCPQVWTSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDMD 340  
Db 216 -----AGVMTLS----- 222  
Qy 341 AVPARRWKEFVRTGLREAEIENVEVE-IGFRDQOQYEMLKRWQ 384



```
Query Match          7.0%; Score 162.5; DB 2; Length 349;
Best Local Similarity 26.7%; Pred. No. 0.00087;
Matches 48; Conservative 21; Mismatches 84; Indels 27; Gaps 10;

QY 15 LLLVLLGARAQGTRSPRCDACGDPFHKKIGLFCRCGCPAGHYLKAPCTPCGNSCLVCP 74
DB 12 LSCIIINGRDAAPYTPPGKCKDTEYKRNHLCCLSCPPGYASRLCDSKT-NTQCTPG 69

QY 75 QDTFLAWENHNHNSCARCOA-CDEQASQVALENCASAVADTRGCKPGFWFVECOVSCVSS 133
DB 70 SGTFTS-RNNHLPACLSNGRCN--SNQVETRSCNTHNRICECSPGYY-----CLKG 119

QY 134 SPFYCQPCLD---CG---ALHRHTRLLCSRRDTCGTCLPGFYEH-----GDCVSCPTST 183
DB 120 GSSGCKACVSOQTKGIGYGVSGHT----SVGDVICSPCGFGTYSHTVSSADKCEPVPNNT 175

RESULT 12
T28623
hypothetical protein G2R - variola major virus
C:Species: variola major virus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28623
R:Masung, R.F.; Eposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: Z20488; MUID:94088747; PMID:8264798
A:Accession: T28623
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <MAS>
A:Cross-references: UNIPROT:P34015; EMBL:L22579; NID:G623595; PIDN:AAA60933.1; PID:G4391
A:Experimental source: strain Bangladesh 1975
C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match          6.9%; Score 159.5; DB 2; Length 348;
Best Local Similarity 26.8%; Pred. No. 0.0014;
Matches 48; Conservative 20; Mismatches 84; Indels 27; Gaps 10;

QY 16 LLLVLLGARAQGTRSPRCDACGDPFHKKIGLFCRCGCPAGHYLKAPCTPCGNSCLVCPQ 75
DB 12 LSCIIINGRDAAPYTPPGKCKDTEYKRNHLCCLSCPPGYASRLCDSKT-NTQCTPGS 69

QY 76 DTFLEWENHNHNSCARCOA-CDEQASQVALENCASAVADTRCGCKPGFWFVECOVSCVSS 134
DB 70 GTFTS-RNNHLPACLSNGRCN--SNQVETRSCNTHNRICECSPGYY-----CLKG 119

QY 135 PFYCQPCLD---CG---ALHRHTRLLCSRRDTCGTCLPGFYEH-----GDCVSCPTST 183
DB 120 SSGCKACVSOQTKGIGYGVSGHT----SVGDVICSPCGFGTYSHTVSSADKCEPVPNNT 174

RESULT 13
A26431
nerve growth factor receptor precursor, low affinity - rat
A:Alternate names: NGF receptor
R:Metzger, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A26431; PH1229
R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115859; PMID:3027580
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
A:Cross-references: UNIPROT:P07174; GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756
R:Metzger, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoid
A:Reference number: PH1229; MUID:93077038; PMID:1446821
A:Accession: PH1229
A:Molecule type: DNA
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A:Residues: 1-20 <MET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma ce
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of t
C:Comment: This protein is thought to form a high-affinity receptor when it associates w
C:Genetics:
A:Introns: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-425/Product: nerve growth factor receptor #status predicted <EXT>
F:30-253/Domain: extracellular #status predicted <EXT>
F:33-66/Domain: NGF receptor repeat homology <NG1>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-148/Domain: NGF receptor repeat homology <NG3>
F:150-190/Domain: NGF receptor repeat homology <NG4>
F:198-249/Region: serine/threonine-rich
F:252-273/Domain: transmembrane #status predicted <MEM>
F:274-425/Domain: intracellular #status predicted <INT>
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          6.8%; Score 158; DB 1; Length 425;
Best Local Similarity 21.2%; Pred. No. 0.0021;
Matches 102; Conservative 42; Mismatches 202; Indels 136; Gaps 21;

QY 1 MEQPRGCAAV--AAALLVLLGARAQGTSPRCDACGDPFHKKIGLFCRCGCPAGHYLK 58
DB 1 MRRAGAACSAMDRLRLLLLTILGV-SGGAKE---TCSTGLYTHSG-ECCKACNLGEGVA 55

QY 59 APC-----TEPCGNSCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASAVD 112
DB 56 QPCGANQTVCEPCLDN---VTFSDVVSATE-----PCKPCTECIGLQMSA--PCVEADD 105

QY 113 TRCCKPGWFE-----CQVSQCVSSSPFYCQPCLDCCGALHRRHTRLLCSRRDTCGT 164
DB 106 AVCRCAYGYQDETGHCACSVCEVSGLVFSQ-----DKQNTVCEE 149

QY 165 CLPGFY----EHGDCVSCPT-----STLGSCTPCRCAAVCGWRQMFVQVLLAGLVVPLL 215
DB 150 CPEGTYSDEANHVDPCLPCTVCEDETERQLRECTPWADAECEIIPGRWI----- 197

QY 216 LGATLTYRHCHWPKPLVTADEAGMEALTP-----PPATHSLPLDLSAHTLLAPPDSS 268
DB 198 -----PRSTPE--GSDSTAPSTOEPEVFPEDQLVPSTVADMTVTVMGSS 240

QY 269 EKICTVLQVGNSTPGYPETOEA---LCPQVTVS--WDQLPSRALGPAAAPTLSPEPAG 323
DB 241 QPVVTRGTTDN-LIPVYCSILAAVVVGLVAVIAFKWNKSKONKOGANSRPNQTPPEG 299

QY 324 -----SPAMMLQPGFQLY-----DVMDAVPARRWKE 349
DB 300 EKLHSDSGISVDSQSLHDQQTHTQTASQALKGDGNYSSLPKREEVEKLLNGDTWRH 359

QY 350 FVRTILGLREARIEAVEVEIGFRDQOYEMLEKRWQQQAGVAVYAAALERMGLDGCVEDL 409
DB 360 LAGELGYQPEHIDSFTHACVPR-----ALLASWGAQDSATLDALLAARRIQRADIVESL 415

QY 410 RS 411
DB 416 CS 417

RESULT 14
T13954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13954
R:Nakajima, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T13954
```



A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1574 <NAK>  
A:Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:93449293; PIDN:BAA32462.1; PID:93449293  
A:Experimental source: strain Sprague-Dawley; brain  
C:Genetics:  
A:Gene: MEGF6

Query Match 6.8%; Score 158; DB 2; Length 1574;  
Best Local Similarity 24.5%; Pred. No. 0.0072;  
Matches 90; Conservative 16; Mismatches 120; Indels 142; Gaps 23;  
Qy 30 SPRCDACGDFHKKIGLFCRCPCAGHY-----LKAPECTPCGNSCLV----- 72  
Db 933 SGACTCPAGWR--GSFCEHACPAAGFFGLDCDSACNSAGAPCDVAVTGSCICPAGRWGPR 989  
Qy 73 ----CPQDTFLAWENHNSECARQACDEQASQVALENCNSAVADTRCCKPGWF----- 122  
Db 990 CAQSCPPPLTF-----GLNCSQICTCFNGAS-----CDSVTG-QCHCAPGMWGPTCLQ 1035  
Qy 123 -----VEQVSOVSSSPFYCOPCL-DCGALHRRHRLLCSSRDTCGTCLPGFYE-- 171  
Db 1036 ACPGLYKKNQHS-CLCRNGRCRDPILGQCTCEGWTGLACENE-----CLPGHYAAG 1088  
Qy 172 -----HGDGC-----VSCPTSTLG-SCPERRCA-----AVC----- 195  
Db 1089 COLNCSLHGGICDLRLTGCHCLCPAGWTGDKCQSSCVSGTFGVHCEHCACRKGASCHHVT 1148  
Qy 196 -----GWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADEAGMALTPPP 248  
Db 1149 GACFCPPGWRGPHCEQAQCPRWGFEACAQRCLCPETNASC--HH--VTG-----ECRCPPG 1199  
Qy 249 ATHLSPLDSANTLLAPPDSSSEKICTVQLVGNWSWTPG-YPETQEAL--CPQVTSMDQLPS 305  
Db 1200 FTGL-----SCEQAC-----QPGTFGKDCHELCQCPGETWACD--PA 1234  
Qy 306 RALGPFAA 313  
Db 1235 SGVCTCAA 1242

RESULT 15  
GQHUN  
nerve growth factor receptor precursor, low affinity [validated] - human  
N:Alternate names: NGF receptor  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text\_change 09-Jul-2004  
C:Accession: A25218; A60204; S21689; I57638  
R:Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.  
Cell 47, 545-554, 1986  
A:Title: Expression and structure of the human NGF receptor.  
A:Reference number: A25218; MUID:87051725; PMID:3022937  
A:Accession: A25218  
A:Molecule type: mRNA  
A:Residues: 1-427 <JOH>  
A:Cross-references: UNIPROT:P08138; GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205  
R:Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.; J. Neurochem. 48, 225-232, 1987  
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor  
A:Reference number: A60204; MUID:87085574; PMID:3025363  
A:Accession: A60204  
A:Molecule type: protein  
A:Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>  
A:Experimental source: melanoma cell line A875  
R:Visavajjalana, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.  
Arch. Biochem. Biophys. 294, 244-252, 1992  
A:Title: Structural domains of the extracellular domain of human nerve growth factor receptor  
A:Reference number: S21689; MUID:92198017; PMID:1372492  
A:Accession: S21689  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 183-208 <VIS>

R;Sehgal, A.; Patil, N.; Chao, M.  
Mol. Cell. Biol. 8, 3160-3167, 1988  
A:Title: A constitutive promoter directs expression of the nerve growth factor receptor (NGF-R) in a variety of cell types.  
A:Reference number: I57638; MUID:89096903; PMID:2850481  
A:Accession: I57638  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-22 <RES>  
A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA3633.1; PID:g189207  
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells, and on a variety of other cell types. The cytosolic domain may form part or all of a complex with the extracellular domain. This protein is thought to form a high-affinity receptor when it associates with the extracellular domain. This receptor undergoes both N- and O-linked glycosylation.  
C:Genetics:  
A:Gene: GDNF  
A:Cross-references: GDB:I20234; OMIM:162010  
A:Map position: 17q21-17q22  
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; tyrosine kinase  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-427/Product: nerve growth factor receptor #status experimental <MAT>  
F:29-250/Domain: extracellular #status predicted <EXT>  
F:32-65/Domain: NGF receptor repeat homology <NG1>  
F:67-108/Domain: NGF receptor repeat homology <NG2>  
F:109-147/Domain: NGF receptor repeat homology <NG3>  
F:149-189/Domain: NGF receptor repeat homology <NG4>  
F:197-248/Region: serine/threonine-rich  
F:251-272/Domain: transmembrane #status predicted <TRM>  
F:273-427/Domain: intracellular #status predicted <INT>  
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.7%; Score 155.5; DB 1; Length 427;  
Best Local Similarity 22.1%; Pred. No. 0.0031;  
Matches 104; Conservative 191; Mismatches 139; Indels 139; Gaps 21;  
Qy 15 LLLVLLGAGGGRSPRCDCAGDFHKKIGLFCRCPCAGHYKAPC-----TEPCNS 68  
Db 16 LLLLLLGV-SLGGAKA--CPTGLYTHSG-ECCKACNLGEGVAQPCGANTVCEPCLD 70  
Qy 69 TCVCPQDTFLAWENHNSECARQACDEQASQVALENCNSA-----VADTRCGCKPGWFVE 124  
Db 71 ---VTFSDVVSATE-----PCKPCTEC-----VGLQMSAPCVCVEADDAVCRCAVGYQD 116  
Qy 125 -----COVSQCVSSSPFYCOPCLDCGALHRRHRLLCSSRDTCGTCLPGFY-----EH 172  
Db 117 ETGRCACRCVCEAGSGLVFSQ-----DKQNTVCECPDGTYSDEANH 160  
Qy 173 GDGCVSCPT-----STLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHC 227  
Db 161 VDPCLPCTVCEDTERQLRECTRWADAECBEIPGRWIT----- 197  
Qy 228 WPHKPLVTADEAGMEALTP--PPATHLSPLDSANTLLAPPDSSSEKICTVQLVGNWSWTPGY 285  
Db 198 -RSTPPEGSSTAPSTOEPEAPPEQDLIASTVAGVTTVMGSSQPVVTRGTTDN-LIPVY 255  
Qy 286 PETQEAL-----CPQVTSMDQLPSRALGPFAAAPTLLSPESPAGSPAMML- 329  
Db 256 CSLAAVVGVLVAVIAFKRWNSCKQNGANSRPNVTPPPEGEKLSHDSGISVDSQSLH 315  
Qy 330 --QPGPQ-----LYDVMDVAVPARR-----WKFEVRTLGLREAEI 361  
Db 316 DQPHPTQTASGQALKGDGGLYSSLP--PAKREEVEKLNGSAGDTWRHLAGELGYQYQPEHI 373  
Qy 362 EAVEVEIGRFRDQOQYEMKRWQOQAPGLGAVVAALERMGLDGCVEILRS 411  
Db 374 DPFTHACPVPR-----ALLASWATQDSATLDALLAALRIQRAIDLVESLCS 419

Search completed: June 27, 2005, 13:40:44  
Job time : 21 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2005, 13:37:13 ; Search time 176 Seconds  
(without alignments)

1213.279 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAVAALLLVLL.....ERMGLDGVEDLRSLRQGP 417

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2323	100.0	417	1	TR25_HUMAN	Q93038 h tumor nec
2	1397	60.1	413	2	Q99MM1	Q99mm1 mus musculus
3	1255	54.0	387	2	Q8VD70	Q8vd70 mus musculus
4	415	17.9	461	1	TR1A_PIG	P50555 sus scrofa
5	406.5	17.5	440	2	Q6QHFO	Q6chf0 mus musculus
6	405.5	17.5	440	2	Q6QHf2	Q6chf2 mus musculus
7	404.5	17.4	440	2	Q6QHf1	Q6chf1 mus musculus
8	404.5	17.4	454	1	TR1A_MOUSE	P25118 mus musculus
9	394.5	17.0	461	1	TR1A_RAT	P22934 rattus norv
10	387.5	16.7	471	1	TR1A_BOVIN	O19131 bos taurus
11	374	16.1	455	1	TR1A_HUMAN	P19438 homo sapien
12	365	15.7	446	2	Q95ND3	Q95nd3 felis silve
13	247.5	10.7	332	1	TRN6_PIG	Q77736 sus scrofa
14	226	9.7	319	2	Q9TV79	Q9tv79 oryctolagus
15	223.5	9.6	389	2	Q6NUU6	Q6nuu6 brachydanio
16	221	9.5	314	2	Q861W6	Q861w6 felis silve
17	217.5	9.4	320	2	Q9XS29	Q9xs29 oryctolagus
18	214.5	9.2	328	2	Q76B99	Q76b99 xenopus lae
19	211.5	9.1	328	2	Q6GLZ4	Q6glz4 xenopus lae
20	206.5	8.9	283	1	TR14_HUMAN	Q92956 homo sapien
21	205	8.8	438	2	Q9DFV0	Q9dfv0 brachydanio
22	203.5	8.8	368	2	Q57408	O57408 meleagris g
23	203.5	8.8	440	1	T10B_HUMAN	O14763 homo sapien
24	200.5	8.6	283	2	Q9XS28	Q9xs28 cercopithec
25	200	8.6	381	1	T10B_MOUSE	Q9qzm4 mus musculus
26	199.5	8.6	335	1	TRN6_HUMAN	P25445 homo sapien
27	193.5	8.6	368	2	Q91AR7	Q91ar7 gallus gall
28	198	8.5	189	2	Q95185	Q95185 felis silve
29	198	8.5	263	2	Q9XS60	Q9xs60 oryctolagus
30	197.5	8.5	276	2	Q71F55	Q71f55 mus musculus
31	197.5	8.5	333	1	TRN6_MACMU	Q9bdp2 macaca mula

32 197 8.5 189 2 097530 canis faml  
33 197 8.5 327 2 097491 ovis aries  
34 196.5 8.5 331 2 0975N4 macaca faec  
35 196 8.4 327 1 TRN6\_MOUSE  
36 195.5 8.4 275 2 Q80W9 mus musculus  
37 195.5 8.4 335 2 Q6SS29  
38 193.5 8.3 331 1 TRN6\_MACNE  
39 193 8.3 334 2 Q9GL40  
40 192.5 8.3 323 1 TRN6\_BOVIN  
41 191 8.2 321 2 Q6DJ81  
42 191 8.2 411 1 Q6UXM8  
43 190.5 8.2 331 1 TRN6\_CERTO  
44 189.5 8.2 368 2 Q9FW79  
45 189 8.1 312 2 Q6E5U7

#### ALIGNMENTS

RESULT 1  
ID TR25\_HUMAN STANDARD; PRT; 417 AA.  
AC Q93038; Q00275; Q00276; Q00277; Q00278; Q00279; Q00280; Q14865;  
AC Q14866; Q78507; P78515; Q29983; Q93036; Q93037; Q99830;  
AC Q99831; Q9BY86; Q9UME0; Q9UME1; Q9UME5;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 25 precursor (WSL-1  
DE protein) (Apoptosis-mediating receptor DR3) (Apoptosis-mediating  
DE receptor TRAMP) (Death domain receptor 3) (WSL protein) (Apoptosis  
DE inducing receptor AIR) (Apo-3) (Lymphocyte associated receptor of  
DE death) (LARD) (UNQ455/PRO779).  
GN Name=TNFRSF25; Synonyms=APO3, DDR3, DR3, TNFRSF12, WSL, WSL1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.  
RC TISSUE=Lymphoid;  
RX MEDLINE=97088617; PubMed=8934525; DOI=10.1038/384372a0;  
RA Kiteon J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,  
RA Grinham C.J., Brown R., Farrow S.N.;  
RA "A death-domain-containing receptor that mediates apoptosis.";  
RA Nature 384:372-375(1996).  
[2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Umbilical vein endothelial cells;  
RX MEDLINE=97081063; PubMed=8875942; DOI=10.1126/science.274.5289.990;  
RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,  
RA Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;  
RA "Signal transduction by DR3, a death domain-containing receptor  
RT related to TNFR-1 and CD95.";  
RT Science 274:990-992(1996).  
[3]  
RN SEQUENCE FROM N.A.  
RP Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;  
RP Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
[4]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Heart;  
RX MEDLINE=97148200; PubMed=8994832; DOI=10.1016/S0960-9822(02)70791-4;  
RA Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,  
RA Goddard A.D., Bauer K.D., Ashkenazi A.;  
RA "Apo-3, a new member of the tumor necrosis factor receptor family,  
RT contains a death domain and activates apoptosis and NF-kappa-B.";  
RT Curr. Biol. 6:1669-1676(1996).  
[5]  
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).  
RX MEDLINE=97272273; PubMed=9114039; DOI=10.1073/pnas.94.9.4615;  
RA Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,  
RA McMichael A.J., Bell J.I.;

RT "LARD: a new lymphoid-specific death domain containing receptor  
RT regulated by alternative pre-mRNA splicing.";  
RL proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).  
RX MEDLINE=98113360; PubMed=9446802; DOI=10.1006/bbrc.1997.7948;  
RA Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,  
RA Salles G.;  
RT "A new death receptor 3 isoform: expression in human lymphoid cell  
RT lines and non-Hodgkin's lymphomas.";  
RL Biochem. Biophys. Res. Commun. 242:376-379(1998).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,  
RA Hayaishi S., Sato M., Shiozawa K., Tsukamoto Y.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Wileand D., Woods K., Xie M.-H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM 11), AND VARIANTS GLN-23; GLY-159 AND  
RP ARG-254.  
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,  
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;  
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department  
RT of Genome Sciences, Seattle, WA (URL: <http://esg.gs.washington.edu>).";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE OF 4-417 FROM N.A.  
RC TISSUE=Brain, and Fetal lung;  
RX MEDLINE=97205335; PubMed=9052839;  
RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,  
RA Thome M., Bornand T., Fahne M., Schroeter M., Wilson A., French L.E.,  
RA Browning J.L., MacDonald H.R., Tschopp J.;  
RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology to  
RT tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";  
RL Immunity 6:79-88(1997).  
RN [11]  
RP SEQUENCE OF 7-417 FROM N.A.  
RC TISSUE=Brain;  
RA Chaudhary P.M., Hood L.E.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP INTERACTION WITH BAG4.  
RX MEDLINE=99115917; PubMed=9915703; DOI=10.1126/science.283.5401.543;  
RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;  
RT "Prevention of constitutive TNF receptor 1 signaling by silencer of  
RT death domains.";  
RL Science 283:543-546(1999).  
RN [13]  
RP SPICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).  
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;  
RA Hillman R.T., Green R.E., Brenner S.E.;  
RT "An unappreciated role for RNA surveillance.";  
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).  
CC -!- FUNCTION: Receptor for TNFSF12/APO3L/TWEAK. Interacts directly  
CC with the adaptor TRADD. Mediates activation of NF-kappa-B and  
CC induces apoptosis. May play a role in regulating lymphocyte  
CC homeostasis.

CC -!- SUBUNIT: Homodimer. Interacts strongly via the death domains with  
CC TNFRSF1 and TRADD to activate at least two distinct signaling  
CC cascades: apoptosis and NF-kappa-B signaling. Interacts with BAG4.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9  
CC and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)  
CC (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=12;  
CC Name=1; Synonyms=WSL-1, LARD-1A;  
CC IsoId=Q93038-1; Sequence=Displayed;  
CC Name=2; Synonyms=LARD-1B;  
CC IsoId=Q93038-2; Sequence=VSP\_006504;  
CC Name=3; Synonyms=WSL-S1, LARD-3;  
CC IsoId=Q93038-3; Sequence=VSP\_006497, VSP\_006498;  
CC Note=May be produced at very low levels due to a premature stop  
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;  
CC Name=4; Synonyms=WSL-S2, LARD-2;  
CC IsoId=Q93038-4; Sequence=VSP\_006501, VSP\_006502;  
CC Note=May be produced at very low levels due to a premature stop  
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;  
CC Name=5; Synonyms=LARD-4, LARD-11;  
CC IsoId=Q93038-5; Sequence=VSP\_006495;  
CC Note=May be produced at very low levels due to a premature stop  
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;  
CC Name=6; Synonyms=LARD-5;  
CC IsoId=Q93038-6; Sequence=VSP\_006491, VSP\_006495;  
CC Note=May be produced at very low levels due to a premature stop  
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;  
CC Name=7; Synonyms=LARD-6;  
CC IsoId=Q93038-7; Sequence=VSP\_006491, VSP\_006493, VSP\_006494;  
CC Note=May be produced at very low levels due to a premature stop  
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;  
CC Name=8; Synonyms=LARD-7;  
CC IsoId=Q93038-8; Sequence=VSP\_006492;  
CC Name=9; Synonyms=LARD-8;  
CC IsoId=Q93038-9; Sequence=VSP\_006491;  
CC Name=10; Synonyms=LARD-9;  
CC IsoId=Q93038-10; Sequence=VSP\_006503;  
CC Name=11; Synonyms=Beta;  
CC IsoId=Q93038-11; Sequence=VSP\_006496;  
CC Name=12; Synonyms=Beta soluble;  
CC IsoId=Q93038-12; Sequence=VSP\_006499, VSP\_006500;  
CC Note=May be produced at very low levels due to a premature stop  
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;  
CC -!- TISSUE SPECIFICITY: Abundantly expressed in thymocytes and  
CC lymphocytes. Detected in lymphocyte-rich tissues such as thymus,  
CC colon, intestine, and spleen. Also found in the prostate.  
CC -!- PTM: Glycosylated (Probable).  
CC -!- SIMILARITY: Contains 1 Death domain.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- CAUTION: Ref.5 reports for isoform 4 at position 208 a serine  
CC residue instead of arginine.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; Y09392; CAA70561.1; -;  
CC EMBL; Y09392; CAA70559.1; -;  
CC EMBL; Y09392; CAA70560.1; -;  
CC EMBL; U72763; AAC50819.1; -;  
CC EMBL; U83599; AAB41434.1; -;  
CC EMBL; U83600; AAB41435.1; -;  
CC EMBL; U78029; AAB40918.1; -;  
CC EMBL; U74611; AAB39714.1; -;  
CC EMBL; U94501; AAC51306.1; -;  
CC EMBL; U94504; AAC51309.1; -;  
CC EMBL; U94502; AAC51307.1; -;  
CC EMBL; U94503; AAC51308.1; -;

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DR EMBL; U94505; AAC51310.1; -
DR EMBL; U94506; AAC51311.1; -
Query Match
  100.0%; Score 2323; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.1e-153; Indels 0; Gaps 0;
Matches 417; Conservative 0; Mismatches 0;
QY 1 MEQPRGCAAAVAAAALLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAAAVAAAALLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKRP 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKRP 120
QY 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180
DB 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQFVQVLLAGLVVPLLLGATLTYYRHCHWPHKPLVTTADEAG 240
DB 181 TSTLGSCPERCAAVCGWRQFVQVLLAGLVVPLLLGATLTYYRHCHWPHKPLVTTADEAG 240
QY 241 MEALTPPPATHLSPDLSAHTLLAPDSSSEKICTVQLVGNWTPGYPETQOALCPQVTTWSW 300
DB 241 MEALTPPPATHLSPDLSAHTLLAPDSSSEKICTVQLVGNWTPGYPETQOALCPQVTTWSW 300
QY 301 DQLPSPRALGPAAPTLSPSPAGSPAMMLQPGPOLYVNDVAVPARRWKEFVRTLGLREAE 360
DB 301 DQLPSPRALGPAAPTLSPSPAGSPAMMLQPGPOLYVNDVAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLVGYAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLVGYAALERMGLDGCVEDLRSRLQRP 417
RESULT 2
Q99MM1 PRELIMINARY; PRT; 413 AA.
AC Q99MM1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE WSL-1-like protein.
GN Name=Tnfrsf25;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
EX MEDLINE=21158384; PubMed=11261933; DOI=10.1007/s002510000290;
RA Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
RA Owen M.J.;
RT "Genomic structure, expression, and chromosome mapping of the mouse
RT homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
RT gene."
RL Immunogenetics 53:59-63(2001).
DR EMBL; AF429969; AAK11256.1; -.
DR HSSP; P19438; 1ICH.
DR MGD; MG1:1934667; Tnfrsf25.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR01029; DEATH-like.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow fac_recept.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
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DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF 2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR 1; UNKNOWN 1.
DR PROSITE; PS00050; TNFR_NGFR 2; 1.
SQ SEQUENCE, 413 AA; 4453 MW; 69F21B85D0DABABF CRC64;
Query Match
  60.1%; Score 1397; DB 2; Length 413;
Best Local Similarity 62.9%; Pred. No. 4.6e-89;
Matches 270; Conservative 28; Mismatches 103; Indels 28; Gaps 7;
QY 1 MEQPRGCAAAVAAAALLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCP 52
DB 1 MEQPRGCAAAVAAAALLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCP 59
QY 53 AGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASAVAD 112
DB 60 KGHYKAPCAEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASAVAD 119
QY 113 TRCGCKPGWFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGT---CLPGF 169
DB 120 THCGCQSGWCDCTVPCGKSPFSCVPCGATTTPVH-----EAPTRPCLPGF 167
QY 170 YEHGDCVSCPTSTLGSCPERCAAVCGWRQFVQVLLAGLVVPLLLGATLTYYRHCHW 229
DB 168 YIRGNDCTSCPTSTLGSCPERCAAVCGWRQFVQVLLAGLVVPLLLGATLTYYRHCHW 224
QY 230 HKPLVTADAEAGMEALTPPPATHLSPDLSAHTLLAPDSSSEKICTVQLVGNWTPGYPET 288
DB 225 CKAVVTADTATEPLASPTAHLASDASNAHTLLAPDSSSTGKICTYVQLVGNWTPGYSQT 284
QY 289 QEALCPQVTTWSWDLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYVNDVAVPARRWK 348
DB 285 QEVVCGQASQPDQLENRTLTGTPLASPLSPAPPAGSPAAVLPQPGPOLYVNDVAVPARRWK 344
QY 349 EFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLVGYAALERMGLDGCVED 408
DB 345 EFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLVGYAALERMGLDGCVED 404
QY 409 LRSRLQRP 417
DB 405 LRSRLQRP 413
RESULT 3
Q8VD70 PRELIMINARY; PRT; 387 AA.
AC Q8VD70;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Tnfrsf25 protein.
GN Name=Tnfrsf25;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017526; AAH17526.1; -.
DR HSP; P19438; 11CH.
DR MGD; MG1:1934667; Tnfrsf25.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 387 AA; 41640 MW; F16644666BAD68D3 CRC64;

Query Match 54.0%; Score 1255; DB 2; Length 387;
Best Local Similarity 57.7%; Pred. No. 3.2e-79;
Matches 248; Conservative 26; Mismatches 92; Indels 64; Gaps 6;

QY 2 EORPRGCAVAAA-----LLLVILGARAQGTSPRCDCAGDPHKKIGLPCC 48
DB 8 ERSPEGAATPGSTARVLQPLFLPLLLLLLLLLGGGQGG-MSGRCDCASESQKRYGPFCC 66
QY 49 RGCPAGHYLKAPCTEPCGNTCLVCPQDTFLAWENHNHNSCARCOACDEQASVALENC 108
DB 67 RGCPKGYWKAPCAEPCGNTCLVCPSTDTFLRDNHFKTDCTRCQVCDEALQVTLNCS 126
QY 109 AVADTRCCCKGWFEVCQVSSPPYCPCLDCGALHRRHLLCSRRDTDCGTCLPG 168
DB 127 AKSDTHCCQCGWCVDCSTPCGKSGSPFCVPGCATTPVH----- 166
QY 169 FVEHGDGCVSPTSLGSCPERCAVCGWRFVQVLLGLVPLLLGATLTYYRHCW 228
DB 167 -----EAPT-----PLFVQVLLG---VAFLEGALLI CAYCRWQ 197
QY 229 PHKPLVTADAGMEALTPPPATHLSPLDSAHTLLAPPDSSBKIC-TVOLVGNSTWPGYPE 287
DB 198 PKAVVTADTAGTETLASPQTAHLSASDSAHTLLAPPSSTGKICTTVQLVGNNTWPGLSQ 257
QY 298 TQEALCPQVTHSWDLPSPALGPAAAPTLSPESPAGSPAMMLQPCPOLYDMDVAVPARRW 347
DB 258 TQEVVCGASQPDQGLPRTLTGTPLASPLSPAPPAGSPAALQPGPOLYDMDVAVPARRW 317
QY 348 KEFVRTLGRAEIEAVEVEIGRFRDQYEMLKRWRQQPAGLGVAVYALERMGLDGCVE 407
DB 318 KEFVRTLGRAEIEAVEVEICRFRDQYEMLKRWRQQPAGLGVAVYALERMGLGCAE 377
QY 408 DLRSRLQRP 417
DB 378 DLRSRLQRP 387

RESULT 4
TRIA_PIG
ID TRIA_PIG STANDARD; PRT; 461 AA.
AC P50555;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-RI) (p55).
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GN OS
OC Eukarya (Pig).
OC Sukrota (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96011645; PubMed=7590278; DOI=10.1016/0378-1119(95)00423-4;
RA Suter B., Pauli U.H.;
RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
RT receptor.";
RL Gene 163:263-266(1995).
CC -1- FUNCTION: Receptor for TNFRSF2/TNF-alpha and homotrimeric
CC TNFRSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC homotrimerization. The aggregated death domains provide a novel
CC molecular interface that interacts specifically with the death
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
CC RIP and possibly FADD, are recruited to the complex by their
CC association with TRADD. This complex activates at least two
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC Binds BAGA. Constitutively associated with TRPC4AP (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: Both the cytoplasmic membrane-proximal region and the C-
CC terminal region containing the death domain are involved in the
CC interaction with TRPC4AP (By similarity).
CC -1- SIMILARITY: Contains 1 death domain.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U19994; AAC48499.1; -.
CC PIR: JC4302; JC4302.
CC HSP; P19438; 11CH.
CC InterPro; IPR000488; Death.
CC InterPro; IPR011029; DEATH like.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00531; Death; 1.
CC Pfam; PF00020; TNFR_C6; 3.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS0017; DEATH DOMAIN; 1.
CC PROSITE; PS00652; TNFR_NGFR_1; 3.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 461 Tumor necrosis factor receptor
FT superfamily member 1A.
FT Extracellular (Potential).
FT Potential.
FT TRANSMEM 211 233 Cytoplasmic (Potential).
FT DOMAIN 234 461 TNFR-Cys 1.
FT REPEAT 43 82 TNFR-Cys 2.
FT REPEAT 83 125 TNFR-Cys 3.
FT REPEAT 126 166 TNFR-Cys 4.
FT REPEAT 167 195 N-SMase activation domain (NSD).
FT DOMAIN 340 350 Death.
FT DOMAIN 362 447 By similarity.
FT DISULFID 44 58 By similarity.
FT DISULFID 59 72 By similarity.
FT DISULFID 62 81 By similarity.
FT DISULFID 84 99 By similarity.
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FT DISULFID 102 117 By similarity.
FT DISULFID 105 125 By similarity.
FT DISULFID 127 143 By similarity.
FT DISULFID 146 158 By similarity.
FT DISULFID 149 166 By similarity.
FT DISULFID 168 179 By similarity.
FT DISULFID 182 194 By similarity.
FT DISULFID 185 190 By similarity.
FT CARBOHYD 54 54 N-linked (GlcNAc...) (potential).
FT CARBOHYD 86 86 N-linked (GlcNAc...) (potential).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (potential).
FT CARBOHYD 151 151 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 461 AA; 50696 MW; CD2361EC60C9D43 CRC64;

Query Match
Best Local Similarity 17.9%; Score 415; DB 1; Length 461;
Matches 140; Conservative 44; Mismatches 201; Indels 74; Gaps 18;

QY 11 VAAALLLVLLGARAQ-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCT 62
DB 14 VLRALLVDVYPAGVHGLVHPGDKRESLCPQGKYSHPNRISICTKCHKGTYLHNDCL 73
QY 63 EPCGNSTCLVCPQDTFLAWENHNSECARCOACDQASQVALENCASAVADTRCGCKPGWF 122
DB 74 GPGLDTRCDUNGFTTASEN-HLTQCLSCSKRSEMSQVEISPTCDRDTVCGCRKN-- 130
QY 123 VECQVSCVSSPFYCPCLDCGALHRRHRLTLC-SRRDTCGTCLPGFYEHGDCGVCSCPT 181
DB 131 ---QYRKYWSETLFOCLNCSLCP--NGTVQLPCLEKQDTIC-NCHSGFFLRDKCEKVCVSN 184
QY 182 STLGCSPERCACVAGWRMP-----WQVLLAGLVVPLLGLATLYTRHCHWPH--- 230
DB 185 CKNADCKNLCPATSETRNDFTGTGTVLLPLVIFFGCLAFPLFVGLACRYQRWKPKLYS 244
QY 231 -----KPLATADAGMEALTPPAPATHLSPLD--SAHTLAPDSDSEKICTV 274
DB 245 IICGKSTPVKEGEPEPLATAPSG-----PITTFSPISFSPPTTFSPVPSFSPISPP 297
QY 275 QLVGNSWT---PGYPETOALCPQVTSWQDQLPSRALGPAAPTLSP-----ESPAG 323
DB 298 TFTPDCWSNIKVTSPPKEIAPPQAG-----PILPMPASTPVPVTPLPKNGGSAHSAHS 352
QY 324 SPAMMLQGP-QLYDMDAVPARRWKEFVRTGLREABIEAVEIGR-FRDOQYEMLMKR 381
DB 353 APAQLADADPATLYAVVDGVPPTRWKEFVRRLGLSEHEIERLELQNGRCLREAQYSLAE 412
QY 382 WRQ---QQPAGIGAVYAALERMGLDGCVEDLRSRLQGP 417
DB 413 WRRRTSRREATLELGSVLRMDMLGCLDEDIEAL-RGP 450

RESULT 5
Q6QHF0 PRELIMINARY; PRT; 440 AA.
AC Q6QHF0
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE TNF receptor superfamily, member 1A (Fragment).
GN Name=Thrsfia,
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Jico; TISSUE=Liver;
RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY541590; AAS48429.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0036021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
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DR GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
DR GO; GO:0008219; P:cell death; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu...; IMP.
DR GO; GO:0006952; P:defense response; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0007242; P:intracellular signaling cascade; TAS.
DR GO; GO:0007515; P:lymph gland development; IMP.
DR GO; GO:0006693; P:prostaglandin metabolism; TAS.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
DR Receptor.
KW NON_TER 1 1
FT NON_TER 440 440
SQ SEQUENCE 440 AA; 48639 MW; D343ED49B260188 CRC64;

Query Match
Best Local Similarity 17.5%; Score 406.5; DB 2; Length 440;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 18;

QY 11 VAAALLLVLLGARAQGGT-----RSPRCDCAGDFHKKIGLFCRCGCPAGHYLKA 59
DB 5 LSLVLLALLMGIIHPSGVGTGLVPSLGDREKRDLSLCPQGKYVHSKNSICTCHKGTLYLS 64
QY 60 PCTPFCNSTCLVCPQDTFLAWENHNSECARCOACDQASQVALENCASAVADTRCGCKP 119
DB 65 DCPSPGRDITVCRECEKGTFTASQNYLR-QCLSCKTCRKEMSQVEISPCQADKDTVCGCK- 122
QY 120 GWFVECVSCVSSPFYCPCLDCGALHRRHRLTLCSSRRDTCGTCLPGFYEHGDCGVCSC 179
DB 123 ---ENQFQYLSETHQCVDCSPC--FNGVTTPCKETQNTVNCNCHAGFFLRSECVPC 176
QY 180 PTSTLGSCTP--ERCAAVC-----GWRQMFVQVLLAGLVVPLLGLATLYTY 224
DB 177 -----SHCKKNECMKCLPPLPLANVTNPQDSGTAVLLPLVLLGLCLSLFIFSLMCRY 231
QY 225 RHCWP-----HKPLVTADAGMEALTPPAPATHLSPLDLSAHTLL-----APDSEK 270
DB 232 PRWRPEVYIIICRDPVPVKEEKAGKPLTPAPSPAFSPSTSGFNPTLGFSTPGFSFVSSTP 291
QY 271 ICTVLQVGNW-----TPGY-PETOALC---PQVTSWQDQLPSRALGPAAP 314
DB 292 ISPI-FGFSNWHXMPVSEVVPTQADPLLYESLCFVPAPTSVQKNE----- 338
QY 315 TLPSPSPAGSPAMMLQGPQLYDMDAVPARRWKEFVRTGLREABIEAVEIGR-FRD 373
DB 339 SAHPQRPVNADLAI-----LYAVVDGVPVPAWKKEFRMGLSEHEIERLEMQNGRCLRE 392
QY 374 QOYEMLMKRQOQPA---GLGAVYAALERMGLDGCVEDLRSRLQGP 417
DB 393 AQYSMLEAWRRRTPRHEDTLEVVGLVLSKMNLAGCLNLEAL-RNP 438

RESULT 6
Q6QHF2 PRELIMINARY; PRT; 440 AA.
AC Q6QHF2
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE TNF receptor superfamily, member 1A (Fragment).
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DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00117; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGR1; 3.
DR PROSITE; PS00500; TNFR_NGR2; 3.
KW Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 454 Tumor necrosis factor receptor
FT FT superfamily member 1A.
FT FT Extracellular (Potential).
FT FT POTENTIAL.
FT FT Cytosolic (Potential).
FT FT TNFR-Cys 1.
FT FT TNFR-Cys 2.
FT FT TNFR-Cys 3.
FT FT TNFR-Cys 4.
FT FT N-SHase activation domain (NSD).
FT FT Death.
FT FT 22 212
FT FT 213 235
FT FT TRANSMEM
FT FT 236 454
FT FT REPEAT 43 82
FT FT REPEAT 83 125
FT FT REPEAT 126 166
FT FT REPEAT 167 196
FT FT 339 349
FT FT 356 441
FT FT 44 58
FT FT DISULFID 59 72
FT FT DISULFID 62 81
FT FT DISULFID 84 99
FT FT DISULFID 102 117
FT FT DISULFID 105 125
FT FT DISULFID 127 143
FT FT DISULFID 146 158
FT FT DISULFID 149 166
FT FT DISULFID 168 179
FT FT DISULFID 182 195
FT FT DISULFID 185 191
FT FT CARBOHYD 54 54
FT FT CARBOHYD 151 151
FT FT CARBOHYD 202 202
FT FT CONFLICT 394 394
FT FT CONFLICT 454 AA; 50129 MW; 0710C2E8C3C286D9 CRC64;
SQ SEQUENCE 17.4%; Score 404.5; DB 1; Length 454;
Best Local Similarity 27.2%; Pred. No. 4.7e-20;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 16;

QY 11 VAAALLVLLGARAAGGT-----RSPRCDCAGDFHKKGLFCRCRCPAGHYLKA 59
DB 11 LSLVLLALLGHHGSGVTLGVPSLGDREKRSCLPCQGGKYVSHSKNSICCTCKHGTLYLS 70
QY 60 PCTEPCGNSTCLVCPQDTFFLAWENHNSECARQACQASQVALENGSAVADTRCGCKP 119
DB 71 DCPSPGRDTCRECEKGTFTASQVLR-QCLSKCTCKEMSQVEISPCQADKDVCGCK- 128
QY 120 GWFVECVQSVSSPPFYCQPCLDGALHRRHLLCSRRDTDCGTCLPGFVEHGDGVCSC 179
DB 129 ----ENQFQVLSETHFQVDCSPC--FNGVTVPICKETQNTVCNCHAGFFLRESECVPC 182
QY 180 PTLTGLSCP--ERCNAVC-----GWQMFVQVLLAGLVPLLLGATLITYY 224
DB 183 ----SHCKNKECKMLCPPLANVTNPQDSGTAVLLPLVLLGLCLLSFFITSLMCRY 237
QY 225 RHCWP-----HKPLVTVADAGMEALTPPATLHSLDLSAHTLL-----APPDSSEK 270
DB 238 PRWRPEVYSIICRDPVPVKEEKAGKPLTPASPAFSTSGFNPTLGFSTPGFSPVSTP 297
QY 271 ICTVLQVNSW-----TPGY-PETQALC-----PQVTSWDLPSRALGPAAAP 314
DB 298 ISPI-FGSPNNHFMFPVSEVVTQCADPLLYESLCSVPAPTSQVKWED----- 344
QY 315 TLPSPSPAGSPAMMLQPGPOLQYDMDVAPARWKEFVTLGLREAEIARVEIGR-PRD 373
DB 345 SAHPORPNADLAI-----LYAVVDGVPPARWKEFMFMGLSHSEIIRLEWMQGRCLRE 398
QY 374 QQYEMLKRWQOOPA--GLGAVVAALERMGLDGCVEDLRSRLQKGP 417
DB 399 AQYSMLAEWRRTTPRHEDTLEVVGLVLSKMNLAGLLENILEAL-RNP 444
RESULT 9

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TR1A RAT
ID TRIA RAT STANDARD; PRT; 461 AA.
AC P22934; Q91V30; Q91V93;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN Name=TNfrsfla; Synonym=TNfr-1, TNfr1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. MEDLINE=1702293;
RX Hammler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor necrosis
RT factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
RC STRAIN=ACI/SegHsd, BBIDR/Wor, BN/SSNHsd, DA/Bkl, F344/NHsd, and
RC LEW/NHsd;
RA Furuya T., Saitstrom J.L., Bina J., Hashimoto A., Dobbins D.E.,
RA Wilder R.L., Remmers E.F.;
RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus
RT among autoimmune susceptible and resistant inbred rat strains.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC homotrimerization. The aggregated death domains provide a novel
CC molecular interface that interacts specifically with the death
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
CC RIP and possibly FADD, are recruited to the complex by their
CC association with TRADD. This complex activates at least two
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC Binds BAGA (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M63122; AAA42256.1; -
DR EMBL; AF329976; AAK53562.1; -
DR EMBL; AF329977; AAK53563.1; -
DR EMBL; AF329981; AAK53567.1; -
DR EMBL; AF329978; AAK53564.1; -
DR EMBL; AF329979; AAK53565.1; -
DR EMBL; AF329980; AAK53566.1; -
DR PIR; B36555; GQRTT1.
DR HSP; P19438; L1CH.
DR RGD; 621237; TNfrsfla.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00005; DEATH; 1.

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FT CHAIN 22 471 Tumor necrosis factor receptor
FT DOMAIN 22 210 superfamily member 1A.
FT TRANSMEM 211 233 Extracellular (Potential).
FT DOMAIN 234 471 Potential.
FT REPEAT 43 82 Cytoplasmic (Potential).
FT REPEAT 83 125 TNFR-Cys 1.
FT REPEAT 126 166 TNFR-Cys 2.
FT REPEAT 167 195 TNFR-Cys 3.
FT REPEAT 196 340 TNFR-Cys 4.
FT DOMAIN 340 360 N-SHase activation domain (NSD).
FT DOMAIN 372 457 Death.
FT DISULFID 44 58 By similarity.
FT DISULFID 59 72 By similarity.
FT DISULFID 62 81 By similarity.
FT DISULFID 84 99 By similarity.
FT DISULFID 102 117 By similarity.
FT DISULFID 105 125 By similarity.
FT DISULFID 127 143 By similarity.
FT DISULFID 146 158 By similarity.
FT DISULFID 149 166 By similarity.
FT DISULFID 168 179 By similarity.
FT DISULFID 182 194 By similarity.
FT DISULFID 185 190 By similarity.
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 471 AA; 51367 MW; 5243BF514DFE81C4 CRC64;

Query Match 16.7%; Score 387.5; DB 1; Length 471;
Best Local Similarity 26.9%; Pred. No. 7.3e-19;
Matches 130; Conservative 47; Mismatches 186; Indels 121; Gaps 18;

QY 11 VAAALLLVLLGARAGGGTRSPRCDCAGDF-----HKIGLFCRCGCPAGHYL 57
Db 14 VLPALLADYVAGVQGLVPH-----GDLEKRESPCGKXNHFNQSTICTCKHGYL 68
QY 58 KAPCTEPCGNTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENSAVADTRCG 117
Db 69 YNDCPGPRDTCRVCAPTGYTALENHLR-RCLSCRCRDEMFOVEISPCVVDRTVCGC 127
QY 118 KPGHFEVCQVQSSSPFYCPCLDC--GALHRRHLLC-SRDTDCGTCLPGFYEHGD 174
Db 128 RKN-----QYREYWGEGTFRCLNCLSLCPNGTVN----IPQERQDTTC-HCHMGFFLKGA 177
QY 175 GCVSCPTSLGSCPER-CAAVCGWR-----QMFVQVLLAGLVPLLLGATLT 221
Db 178 KICSC-----HDCNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASASVULA 232
QY 222 YTYRHCWPHK-----PLVT 235
Db 233 CRYQR-WKPKLYSIICQSTLVKEGEPPELLVPAPGNFTTTCFSSPTSSPVSIIPVIS 291
QY 236 ADEAGMEALTTPPATHLSPLDSANTHLLAPPSSSEKICTVQLVGNSS--WTPGYPTQALC 293
Db 292 CDRENFGAVAPSSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCT 351
QY 294 FOVTSWNPQLSRALGAAAFTLPSPSPAGSPAMMLQPGPOLYDMDVAPARRKKEFVRT 353
Db 352 PVQKW-----EASAPSAQPLADADPA-----TLYAVVDGVPSPRWKELVRR 393
QY 354 LGLREAEIEAVEVEIGR-FRQQQYEMLKRWRQQQP---AGLGAVYAALERMGLDCGVEDL 409
Db 394 LGLSEHEIERLENGRHLREAQYSLAAWRRRTTREATUELLGRVLRDMDLLGCLNI 453
QY 410 RSRL 413
Db 454 EAL 457

RESULT 11
TRIA_HUMAN
ID TRIA_HUMAN STANDARD; PRT; 455 AA.
AC P19438;
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DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55) (CD120a) [Contains: Tumor necrosis factor
DE binding protein 1 (TBPI)].
DE Name=TNFRSF1A; Synonyms=TNFAR, TNFR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90235285; PubMed=2158863;
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;
RT "Molecular cloning and expression of a receptor for human tumor
RL necrosis factor.";
RL Cell 61:361-370(1990).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=90235284; PubMed=2158862;
RA Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
RA Tabuchi H., Lesslauer W.;
RT "Molecular cloning and expression of the human 55 kd tumor necrosis
RT factor receptor.";
RL Cell 61:351-359(1990).
RN [3]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX MEDLINE=91006021; PubMed=1698610;
RA Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,
RA Aderka D., Holtmann H., Wallach D.;
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT for the type I TNF-R, cloned using amino acid sequence data of its
RT soluble form, encodes both the cell surface and a soluble form of the
RT receptor.";
RL EMBO J. 9:3269-3278(1990).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=91090841; PubMed=1702293;
RA Hammler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor necrosis
RT factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
RN [5]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91017509; PubMed=2170974;
RA Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
RT expression of recombinant soluble TNF-binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RN [6]
RN SEQUENCE FROM N.A.
RX MEDLINE=9250049; PubMed=1315717;
RA Fuchs P., Strehl S., Dworzak M., Himmeler A., Ambros P.F.;
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RT localization to chromosome 12p13.";
RL Genomics 13:219-224(1992).
RN [7]
RN SEQUENCE FROM N.A., AND VARIANTS LEU-75 AND GLN-121.
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,
RA Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL6682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu.);
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RN SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
RA Paney J., Helton E., Kettunen M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Trichman J.W., Green E.D., Dickens M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[9]  
RP SEQUENCE OF 41-45.  
RP MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human urine.  
RT Evidence for immunological cross-reactivity with cell surface tumor  
RT necrosis factor receptors.";  
RL J. Biol. Chem. 265:1531-1536 (1990).  
[10]  
RP INTERACTION WITH BAG4.  
RP MEDLINE=91115917; PubMed=9915703; DOI=10.1126/science.283.5401.543;  
RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;  
RT "Prevention of constitutive TNF receptor 1 signaling by silencer of  
RT death domains.";  
RL Science 283:543-546 (1999).  
[11]  
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFBS.  
RP MEDLINE=93258809; PubMed=8387891; DOI=10.1016/0092-8674(93)90132-A;  
RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,  
RA Broger C., Loetscher H., Lesslauer W.;  
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
RT beta complex: implications for TNF receptor activation.";  
RL Cell 73:431-445 (1993).  
[12]  
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
RP MEDLINE=97094982; PubMed=8939750;  
RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;  
RT "Structures of the extracellular domain of the type I tumor necrosis  
RT factor receptor.";  
RL Structure 4:1251-1262 (1996).  
[13]  
RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.  
RA MEDLINE=99213501; PubMed=1019409; DOI=10.1016/S0092-8674(00)80721-7;  
RA McDermott M.F., Akentjevich I., Galon J., McDermott E.M.,  
RA Ogunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko L.,  
RA Petherick T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,  
RA Teppo A.-M., Wilson M., Karaaslan H.M., Wan Y., Todd I., Wood G.,  
RA Schlimgen R., Kumarajeewa T.R., Cooper S.M., Vella J.P., Amos C.I.,  
RA Mulley J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,  
RA Hitman G.A., O'Shea J., Kastner D.L.;  
RT "Germline mutations in the extracellular domains of the 55 kDa TNF  
RT receptor, TNFR1, define a family of dominantly inherited  
RT autoinflammatory syndromes.";  
RL Cell 97:133-144 (1999).  
[14]  
RP VARIANT FHF SER-59.  
RA PubMed=10902757;  
RA Dode C., Papo T., Fieschi C., Pecheux C., Dion E., Picard F.,  
RA Godeau P., Bienvenu J., Piette J.C., Delpech M., Grateau G.;  
RT "A novel missense mutation (C30S) in the gene encoding tumor necrosis  
RT factor receptor 1 linked to autosomal-dominant recurrent fever with  
RT localized myositis in a French family.";  
RL Arthritis Rheum. 43:1535-1542 (2000).

RN VARIANTS FHF GLN-51; SER-59; GLY-62; LEU-75; GLY-115 AND GLN-121.  
RX PubMed=11443543;  
RA Akentjevich I., Galon J., Soares M., Mansfield E., Hull K.,  
RA Oh H.-H., Goldbach-Mansky R., Dean J., Athreya B., Reginato A.J.,  
RA Henrickson M., Fong-Estel B., O'Shea J.J., Kastner D.L.;  
RT "The tumor-necrosis-factor receptor-associated periodic syndrome: new  
RT mutations in TNFRSF1A, ancestral origins, genotype-phenotype studies,  
RT and evidence for further genetic heterogeneity of periodic fevers.";  
RL Am. J. Hum. Genet. 69:301-314 (2001).  
[16]  
RP VARIANTS FHF SER-99 AND PRO-121.  
RX PubMed=13130484; DOI=10.1002/art.11215;  
RA Aganna E., Hammond L., Hawkins P.N., Aldea A., McKee S.A.,  
RA Ploos van Amstel H.K., Mischung C., Kusuhsara K., Saulsbury F.T.,  
RA Lachmann H.J., Bybee A., McDermott E.M., La Regina M., Arostegui J.I.,  
RA Campistol J.M., Worthington S., High K.P., Molloy M.G., Baker N.,  
RA Bidwell J.L., Castaner J.L., Whiteford M.L., Janssens-Korpola P.L.,  
RA Manna R., Powell R.J., Woo P., Solis P., Minden K., Frenkel J.,  
RA Yague J., Mirakian R.M., Hitman G.A., McDermott M.F.;  
RT "Heterogeneity among patients with tumor necrosis factor receptor-  
RT associated periodic syndrome phenotypes.";  
RL Arthritis Rheum. 48:2632-2644 (2003).  
[17]  
RP VARIANT FHF SER-99.  
RX PubMed=14610673; DOI=10.1007/s00431-003-1338-0;  
RA Kusuhsara K., Nomura A., Nakao F., Hara T.;  
RT "Tumor necrosis factor receptor-associated periodic syndrome with a  
RT novel mutation in the TNFRSF1A gene in a Japanese family.";  
RL Eur. J. Pediatr. 163:30-32 (2004).  
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis. Contributes to  
CC the induction of noncytotoxic TNF effects including anti-viral  
CC state and activation of the acid sphingomyelinase.  
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to  
CC homotrimerization. The aggregated death domains provide a novel  
CC molecular interface that interacts specifically with the death  
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
CC RIP and possibly FADD, are recruited to the complex by their  
CC association with TRADD. This complex activates at least two  
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
CC Binds BAG4. Constitutively associated with TRPC4AP (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
CC -!- DOMAIN: The domain that induces A-SMASE is probably identical to  
CC the death domain. The N-SMASE activation domain (NSD) is both  
CC necessary and sufficient for activation of N-SMASE.  
CC -!- DOMAIN: Both the cytoplasmic membrane-proximal region and the C-  
Query Match 16.1%; Score 374; DB 1; Length 455;  
Best Local Similarity 28.3%; Pred. No. 6.1e-18;  
Matches 131; Conservative 49; Mismatches 183; Indels 100; Gaps 22;  
QY 15 LLLVLLGARAQG-----GTRSPR---CDACGDFHKKIGLFCRCGCPAGHYLKAPCTE 63  
DB 15 LLELVGLVPSGVGLVPLHGDREKRSVCGQGYVHPQNNISICTCKHGTLYNDPCG 74  
QY 64 PCGNSTCLVCPQDTFLAWENHNHSEACRQACDEQAQVALENCASAVATRCGCKPGFWV 123  
DB 75 PGQDTCRECSGSGFTASENHLR-HCLSCSKCKEMGQVEISSCTVDRTVCGCRKNQYR 133  
QY 124 EC---QVSQCVSSSPFYCPCLDCGALHRRHLLCSRDDTCGCTLPCFYEHDGCVSCP 180  
DB 134 HYSENLFQ-----FNCSLCLN-GTVH-----LSCQEKQNTVCTCHAGFFRENECVSC- 182  
QY 181 TSTLGSCPE--RCAAVC-----GWRQMFVQVLLAGLVPLLLGATITYYRH 226  
DB 183 ----SNCKKSECTKLCUPQENVKGTEDSGTVLLPLVIFFGCLLSLLFGLMYRQYR 238

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QY 227 CWPHK-----PLVTADAGMEALTPPPATHLSPLDS-----AHTLLAPPPSSSEKIC 272
Db 239 -WKSXLXIVCGKSPPEKEGEGTTKP---LAPNPSFSTPGFTPLGSPVPSSTFT 294
QY 273 TVQLVGNWSTGYPETQALCPQVTSWMDQLPSRALGP-----AAAPTLS- 318
Db 295 S-----SSTYTFGD-----CFNFA-----APPREVAPPYQCADPILATALASDPINPL 338
QY 319 ---ESPAGSPAMWLQGP-QLYDYMADVAPARRWKEFVRTLGLREAEIEAVEVEIGR-PRD 373
Db 339 QKWEDSAHKPSQDITDDPATIYAVVENVPPRLWKEFVRLGLSDHEIDRLQLONGRCLE 398
QY 374 QQYEMLKWRQOQP---AGLGAVYAALERMGLDGCVEDLRSRL 413
Db 399 AQYSLMATWRRRTPREATLELLGRVLRMDLLGCLDIEAL 441

RESULT 12
ID Q95ND3 PRELIMINARY; PRT; 446 AA.
AC Q95ND3;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Tumor necrosis factor type I.
GN Name=TNFR I;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21425403; PubMed=11531421; DOI=10.1006/viro.2001.1042;
RT Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT "TNF-alpha-induced cell death in feline immunodeficiency virus-
RT infected cells is mediated by the caspase cascade.";
RL Virology 287:446-455(2001).
DR EMBL; AB051103; BAB55455.1; -.
DR HSSP; P19438; 1ICH.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
SQ SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;

Query Match 15.7%; Score 365; DB 2; Length 446;
Best Local Similarity 27.0%; Pred. No. 2.5e-17;
Matches 126; Conservative 45; Mismatches 184; Indels 112; Gaps 19;

QY 11 VAALLVLLGARAQG-----GTRSPRCDCAGDHKKIGLFCRCGCPAGHYLKAPCT 62
Db 14 VLLALLVEIYPLRVTLVPHLRDREKRAIPCCQKYIHPQNSICCTCKHKGTYLYNDCA 73
QY 63 EPGCNSTCLVCPQDTFLAWENHNSCARCOACDEQASVALENCNSAVADPRCGCKPGWF 122
Db 74 GPGLDTCRECENGTFTTASENVLR-QCLSCSKCKEMYQVEISPTVYRDTVCGRKN-- 130
QY 123 VECQSVQCVSSPPYCPQCLDCGALHRRHTRLLCSRRDTCOTCLPGFVHEHGDGCVSPTS 182
Db 131 ---QRYRYWSETHFQCLNCSLC--LNGTVQISCKETQNTVCTCHAGFFLRGNECVSCVNC 185
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QY 183 TLGS-CPERCAAVC-----GWRQMFVQVLLAGLVVPLLAGATLTYTYR----- 225
Db 186 KNTTECKLCPVIVETVKDPQDPQTTVLLPLVIFPGICVLSFSLGMCRYORRRSKULPSI 245
QY 226 ---HCWPHK-----PLVTADAGMEALTPPPATHLSPLDSAHTLLAPPPSSSEKICTVQLV 277
Db 246 VCGKSTPTKEGEPQLATG-----PGFSPISPPTFSP---SPTTSP----- 285
QY 278 GNSWTPGYPETQALCPQVTSWMDQL-----PSRALGP---AAAPTLS- 318
Db 286 ---TFTPS-----DWNALRAASVREMAPPYQAGAPILSAAPASSPSTFVQ 329
QY 319 -----ESPAGSPAMWLQGPOLYDYMADVAPARRWKEFVRTLGLREAEIEAVEVEIGR 370
Db 330 KWEDSTHTQRPADPA---DPA-TLYAVVDGVPSPRWKEFVRLGLSEHIERLELQNGR 385
QY 371 -FRDQYEMLKWRQOQP---AGLGAVYAALERMGLDGCVEDLRSRL 413
Db 386 CLREAHYSMLAAWRRTPREATLELLGRVLRMDLLGCLDIEAL 432

RESULT 13
ID TNR6_PIG STANDARD; PRT; 332 AA.
AC O77736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95 antigen)
GN Name=TNFRSF6; Synonyms=APT1, FAS;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RX "Expression of apoptosis-associated genes in hibernating and stunned
RX myocardium of pig.";
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: Contains a death domain involved in the binding of FADD,
CC and maybe to other cytosolic adaptor proteins.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ001202; CAA04596.1; -.
CC HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
```

```
DR Pfam; PF00020; TNFR_c6; 3.  
DR PRINTS; PRO1680; FASRECEPTOR.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS0017; DEATH DOMAIN; 1.  
DR PROSITE; PS00652; TNFR_NGFR_1; 2.  
DR PROSITE; PS00650; TNFR_NGFR_2; 2.  
KW Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 16  
FT CHAIN 17 332  
FT DOMAIN 17 332  
FT TRANSMEM 17 332  
FT DOMAIN 17 175  
FT TRANSMEM 176 192  
FT REPEAT 45 81  
FT REPEAT 82 125  
FT REPEAT 126 164  
FT DOMAIN 227 311  
FT DISULFID 46 57  
FT DISULFID 58 71  
FT DISULFID 61 80  
FT DISULFID 83 99  
FT DISULFID 102 117  
FT DISULFID 105 125  
FT DISULFID 127 141  
FT DISULFID 144 155  
FT DISULFID 147 163  
FT CARBOHYD 38 38  
FT CARBOHYD 116 116  
SQ SEQUENCE 332 AA; 37592 MW; 598B03682756BF1B CRC64;  
  
Query Match 10.7%; Score 247.5; DB 1; Length 332;  
Best Local Similarity 30.3%; Pred. No. 2.7e-09;  
Matches 56; Conservative 23; Mismatches 67; Indels 39; Gaps 7;  
  
Qy 34 DCAGDFHKKIGLCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARQ 93  
Db 45 ECPGQHRE-GQFCQCPGPKGRKHADCTSPGAPQCPVCEGDEYTDKNHSSKRCR 103  
Qy 94 ACDEQASQVALENSAVADTRCGCKPGFVEVCQVSSPFFVQCPCDCLGALHRL 153  
Db 104 VCDGEHGLEVEKNCRTQNTQTKRCCKNPF--CHTSQCE-----HCNPTTC----- 147  
Qy 154 LCSRRDTCGTLGFGFYHGG--DGCVCPTTLGSCPERCAVCGWRQFVQVLLAGLV 211  
Db 148 -----EHGVIENT--PTSNT-KREVFOAGSRSNLHMLWALLILP 187  
  
Qy 212 VPLLL 216  
Db 188 VPALV 192  
  
RESULT 14  
Q9TV79 PRELIMINARY; PRT; 319 AA.  
AC Q9TV79  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE B-type Fas antigen.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
RX NCBI_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Isono T., Tanabe Y., Nagano Y., Seto A.;  
RL EMBL; AB021298; BAA78430.1; -  
DR EMBL; P25445; 1DDP.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005535; F:protein binding; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
```

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DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR011029; DEATH_like.  
DR InterPro; IPR008063; Fas_receptor.  
DR InterPro; IPR001368; TNFR_c6.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00020; TNFR_c6; 2.  
DR PRINTS; PRO1680; FASRECEPTOR.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS0017; DEATH DOMAIN; 1.  
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.  
DR PROSITE; PS00650; TNFR_NGFR_2; 2.  
SQ SEQUENCE 319 AA; 35961 MW; 06FA0033B1846591 CRC64;  
  
Query Match 9.7%; Score 226; DB 2; Length 319;  
Best Local Similarity 21.0%; Pred. No. 9.2e-08;  
Matches 73; Conservative 42; Mismatches 103; Indels 130; Gaps 12;  
  
Qy 44 GLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQASQVA 103  
Db 41 GNFCQQLCPGCTKKADCTSNEGKPCQEGEYTDKSHFSKCRCSLGDGEGHLEV 100  
Qy 104 LENCASAVADTRCGCKPGFVEVCQVSSPFFVQCPCDCLGALHRLHRLCSRRTDCG 163  
Db 101 ETDCTTQNTKRCCKSNPF--CNALKCE-----HCDPCTMC----- 134  
Qy 164 TCLPGFYHGGDGCVCPTSTLGSCEPCRCNAVCGWRQFVQVLLAGLVVLLGLNTLYT 223  
Db 135 -----EHGI-IBECTQTSNTKCKERGTTGSKHLLFWLSTL---LLIPIVLG----- 177  
Qy 224 YRHCWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNWTP 283  
Db 178 LRRYKGR-----DCKH----- 189  
Qy 284 GYPTQEQALCPQVTSWDQPSRALGPAAP-----TLPSPSPAGSPAMMLQPGPOLYD 337  
Db 190 GYDK-----STALIPEGVPMFSDVDISKYIPT----- 217  
Qy 338 VMDAVPARRWKEFVRTGLREAEIEAVEVE-IGRFROQOYEMLKWRO 384  
Db 218 IAEEMKINEVKEFVRKGVNEAKIDEIKNDNIQDTABQKQLLRNWHQ 265  
  
RESULT 15  
Q6NUU6 PRELIMINARY; PRT; 389 AA.  
AC Q6NUU6  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE ZGC:85914.  
GN ORFNames=zgc:85914;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Danio.  
RX NCBI_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., Mcewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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OM protein - protein search, using sw model

Run on: . June 27, 2005, 13:37:14 ; Search time 164 Seconds  
(without alignments) 983.409 Million cell u

**Title:** US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAAVAAALLVLL.....ERMGLDGCVEDLRSRLQGRP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
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## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	\$			
1	2323	100.0	417	2	AAW31517	Aaw31517 Death dom
2	2323	100.0	417	2	AAW26709	Aaw26709 Human apo
3	2323	100.0	417	2	AAW57045	Aaw57045 Human apo
4	2323	100.0	417	2	AAW95538	Aaw95538 Death dom
5	2323	100.0	417	2	AAW05743	Aay05743 Tumour ne
6	2323	100.0	417	3	AAW36265	Aab36265 Human dea
7	2323	100.0	417	4	AAW97370	Aaw97370 Human rhe
8	2323	100.0	417	5	AAW017879	Aao17879 Human rhe
9	2323	100.0	417	5	AAW86139	Aaw86139 Human PRO
10	2323	100.0	417	6	ABW73993	Abw73993 Human Apo
11	2323	100.0	417	6	ABW08252	Abu08252 Human Apo
12	2323	100.0	417	6	ABW73859	Abw73859 Human foe
13	2323	100.0	417	6	ABU10204	Abu10204 Human Apo
14	2323	100.0	417	6	ADA00738	Ada00738 Human GEN
15	2323	100.0	417	6	ABW73824	Abw73824 Human apo
16	2323	100.0	417	6	ADA49692	Ada49692 Human Apo
17	2323	100.0	417	7	ABW02265	Abw02265 Human TNF
18	2323	100.0	417	7	ABW088381	Abw088381 Human dea
19	2323	100.0	417	7	ADJ37305	Adj37305 Human tum
20	2323	100.0	417	7	ADJ95869	Adj95869 Human BEC
21	2323	100.0	417	8	ADH34623	Adh34623 TNF recepr
22	2323	100.0	417	8	ADG68229	Adg68229 Human PRO
23	2323	100.0	417	8	ADL27893	Adl27893 Human Dea
24	2323	100.0	417	8	ADQ16568	Adq16568 Human dea
25	2323	100.0	417	8	ADO59120	Ado59120 Human dea

## ALIGNMENTS

RESULT 1

RESULT 1  
AAW31517  
ID AAW31517 standard: protein: 417 AA.

AA AAW31517:

XX  
DT 02-MAR-1998 (first entry)

DEATH domain containing receptor DR3.

xx Death domain containing receptor; DR3-V1; human; apoptosis; inflammation;  
kw NF-kappaB.  
kw

XX  
OS  
Homo sapiens.

Key	Location/Qualifiers
Peptide	1..24
FT	/label= Sig_peptide
FT	
FT	25..201
FT	/note= "extracellular domain"
FT	202..224
FT	/note= "transmembrane domain"
FT	225..417
FT	/note= "intracellular domain"
FT	342..408
FT	/note= "death domain"
FT	

XX  
PN  
WO9733904-A1

XX PD 18-SEP-1997

XX 17-OCT-1996: 96WO-US016849. PF

XX  
PR 12-MAR-1996: 96US-0013285P.

XX (HUMA-) HUMAN GENOME SCI INC.  
PA (UNMI) UNIV MICHIGAN.

XX  
PI Yu G. Ni J. Dixit VM. Gentz RL. Dillon PJ:

XX  
DR WPI; 1997-470812/43.

DR N-PSDB; AAT89427.

Death domain containing receptor polypeptide(s) DR3 and DR3-V2 - for activation of apoptosis and NF-kappaB, antagonists can be used to treat inflammatory diseases.

XX  
PS  
Claim 1: Page 75-77; 108pp; English.



Db 301 DQLPSRALGPAAPTLSPEAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTTLGLREAE 360  
QY 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417  
Db 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417  
RESULT 3  
AAW57045  
ID AAW57045 standard; protein; 417 AA.  
AC AAW57045;  
XX  
DT 20-AUG-1998 (first entry)  
XX  
DE Human apoptosis inducing receptor.  
XX  
KW Apoptosis inducing receptor; AIR protein; human; cell death regulator;  
KW Type I transmembrane protein; tumour cell death; autoimmune disease;  
KW therapy.  
XX  
OS Homo sapiens.  
XX  
FW WO9814565-A1.  
XX  
PD 09-APR-1998.  
XX  
PF 03-OCT-1997; 97WO-US017876.  
XX  
PR 04-OCT-1996; 96US-0044456P.  
XX  
PA (IMMV) IMMUNEX CORP.  
XX  
PI Perkins PA;  
XX  
DR WPI; 1998-240077/21.  
DR N-PSDB; AAV28700.  
XX  
PT DNA encoding apoptosis inducing receptor - which is Type I transmembrane  
PT protein, useful for regulating cell death.  
XX  
PS Claim 16; Page 28-30; 45pp; English.  
XX  
CC This sequence is the human apoptosis inducing receptor (AIR) of the  
CC invention. AIR is a Type I transmembrane protein, soluble forms of which  
CC can be used to regulate cell death in a therapeutic setting. Soluble AIR  
CC can also be used in vitro to block apoptosis or AIR-expressing cells, or  
CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain  
CC of AIR can be used to develop assays for inhibitors of AIR-induced cell  
CC death, which is useful to regulate cell death in a therapeutic setting as  
CC well as in vitro. Agonists of AIR activity can be used to kill tumour  
CC cells that express AIR, or T cells expressing AIR in autoimmune diseases  
XX  
SQ Sequence 417 AA;  
Query Match 100.0%; Score 2323; DB 2; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.3e-161;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEQPRGCAAVAAALLLVLLGARAQGGTSPRCDGDFHKKIGLFCRCGCPAGHYLKAP 60  
Db 1 MEQPRGCAAVAAALLLVLLGARAQGGTSPRCDGDFHKKIGLFCRCGCPAGHYLKAP 60  
QY 61 CTEPCGNSTCLVCPDPTFLAWNHNSCARQACDEQASQVALENCASAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPDPTFLAWNHNSCARQACDEQASQVALENCASAVADTRCGCKPG 120  
QY 121 WFVEQVQSCVSSFFYQPCPLDCGALHRTLLCSRRDTCGTCLPGFYEHGDCVSCP 180  
Db 121 WFVEQVQSCVSSFFYQPCPLDCGALHRTLLCSRRDTCGTCLPGFYEHGDCVSCP 180  
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCWPHKPLVTADBAG 240

Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCWPHKPLVTADBAG 240  
QY 241 MEALTTPPATHSLSDSAHTLLAPPDSSEKICTVOLGNSWTPGYPETOEALCPQVTTWSW 300  
Db 241 MEALTTPPATHSLSDSAHTLLAPPDSSEKICTVOLGNSWTPGYPETOEALCPQVTTWSW 300  
QY 301 DQLPSRALGPAAPTLSPEAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTTLGLREAE 360  
Db 301 DQLPSRALGPAAPTLSPEAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTTLGLREAE 360  
QY 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417  
Db 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417  
RESULT 4  
AAW5538  
ID AAW5538 standard; protein; 417 AA.  
XX  
AC AAW5538;  
XX  
DT 25-MAR-1999 (first entry)  
XX  
DE Death domain containing receptor polypeptide (DR3).  
XX  
KW Death domain; receptor; DR3-V1; DR3; recombinant.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT Peptide 1. .24 Location/Qualifiers  
FT Protein 25. .417 /note= "signal peptide"  
FT /note= "mature protein"  
XX  
FN JP11000170-A.  
XX  
PD 06-JAN-1999.  
XX  
PF 12-MAR-1997; 97JP-00057503.  
XX  
PR 12-MAR-1996; 96US-0013285P.  
PR 17-OCT-1996; 96US-0028711P.  
PR 06-FEB-1997; 97US-0037341P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (UNMI) UNIV MICHIGAN.  
XX  
DR WPI; 1999-124390/11.  
DR N-PSDB; AAX00925.  
XX  
PT New death domain containing receptor and recombinant vector - optionally  
PT comprising leader sequence.  
XX  
PS Claim 1; Fig 3; 50pp; Japanese.  
XX  
CC The invention provides nucleotide sequences encoding death domain  
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone is  
CC contained in ATCC deposition No. 97456 and the DR3 cDNA clone is  
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising  
CC the nucleic acid sequences and optionally the leader sequences are used  
CC for the recombinant production of the proteins. The present sequence  
CC represents the amino acid sequence of a death domain containing receptor  
CC polypeptide (DR3)  
XX  
SQ Sequence 417 AA;  
Query Match 100.0%; Score 2323; DB 2; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.3e-161;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEQPRGCAAVAAALLLVLLGARAQGGTSPRCDGDFHKKIGLFCRCGCPAGHYLKAP 60

Db 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Qy 61 CTEPCGNSTCLVCPQDPTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPQDPTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Qy 121 WFVECOVSQCVSSSPFYCQPCDCLGALHHRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180  
Db 121 WFVECOVSQCVSSSPFYCQPCDCLGALHHRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180  
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADREAG 240  
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADREAG 240  
Qy 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWPGYPETQALCPQVTWSW 300  
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWPGYPETQALCPQVTWSW 300  
Qy 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTILGLREAE 360  
Db 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTILGLREAE 360  
Qy 361 IEAVEVEIGRFRDQOQYEMLKRWRQQPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417  
Db 361 IEAVEVEIGRFRDQOQYEMLKRWRQQPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417

RESULT 5  
AAY05743  
ID AAY05743 standard; protein; 417 AA.  
AC AAY05743;  
XX  
DT 19-JUL-1999 (first entry)  
DE Tumour necrosis factor receptor TR3.  
XX  
KW Tumour necrosis factor receptor; TR3; DR3; Apo3; WSL-1; LARD; agonist;  
KW antagonist; screening; human; Alzheimer's disease; AIDS; cancer;  
KW inflammation; arthritis; septicaemia; autoimmune disease; psoriasis;  
KW inflammatory bowel disease; transplant rejection;  
KW graft versus host disease; infection; stroke; ischaemia;  
KW acute respiratory disease syndrome; restenosis; brain injury;  
KW bone disease; atherosclerosis; therapy.  
XX  
OS Homo sapiens.  
XX  
FN EP911633-A1.  
XX  
PD 28-APR-1999.  
XX  
PF 02-OCT-1998; 98EP-00203332.  
XX  
PR 08-OCT-1997; 97US-0061334P.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI McDonnell PC, Young PR, Zou J;  
XX  
DR WPI; 1999-246560/21.  
XX  
PT Identifying agonists and antagonists of tumor necrosis factor related  
PT receptors TR1, TR3 and TR5, and of ligand TL3, useful for treatment of  
PT cancer, AIDS, Alzheimer's disease, bone disease etc.  
XX  
PS Disclosure; Page 12-13; 23pp; English.  
XX  
CC The present sequence represents tumour necrosis factor receptor (TNFR)  
CC TR31, also known as DR3, Apo3, WSL-1 or LARD. The invention relates to  
CC TNFR related polypeptides TR1, TR3 and TR5 (see AAY05742-44) and their  
CC ligand TL3 (see AAY05745). TR1, TR3, TR5 and TL3 are used in claimed  
CC methods of identifying agonists and antagonists, i.e. compounds that bind

CC to the receptors or ligand, and which activate (agonist) or inhibit  
CC activation of (antagonists) TR1, TR3, TR5 or TL3. A screening kit for  
CC identifying agonists, antagonists, ligands, receptors, substrates,  
CC enzymes etc. for TR1, TR3, TR5 or TL3 polypeptides is provided. The  
CC agonists and antagonists are useful for treatment of chronic and acute  
CC inflammation, arthritis, septicaemia, autoimmune disease e.g.  
CC inflammatory bowel disease, psoriasis, transplant rejection, graft versus  
CC host disease, infection, stroke, ischaemia, acute respiratory disease  
CC syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g.  
CC lymphoproliferative disorders), atherosclerosis, Alzheimer's disease,  
CC etc., caused by imbalance of TR1, TR3, TR5 or TL3  
XX  
SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.3e-161;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Db 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Qy 61 CTEPCGNSTCLVCPQDPTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPQDPTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Qy 121 WFVECOVSQCVSSSPFYCQPCDCLGALHHRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180  
Db 121 WFVECOVSQCVSSSPFYCQPCDCLGALHHRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180  
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADREAG 240  
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADREAG 240  
Qy 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWPGYPETQALCPQVTWSW 300  
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWPGYPETQALCPQVTWSW 300  
Qy 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTILGLREAE 360  
Db 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTILGLREAE 360  
Qy 361 IEAVEVEIGRFRDQOQYEMLKRWRQQPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417  
Db 361 IEAVEVEIGRFRDQOQYEMLKRWRQQPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417

RESULT 6  
AAB36265  
ID AAB36265 standard; protein; 417 AA.  
XX  
AC AAB36265;  
XX  
DT 20-FEB-2001 (first entry)  
XX  
DE Human death domain containing receptor DR3.  
XX  
KW Human; death domain containing receptor; DR3; cancer;  
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;  
KW neurodegenerative disease; angiogenesis.  
XX  
OS Homo sapiens.  
XX  
PN WO200064465-A1.  
XX  
PD 02-NOV-2000.  
XX  
PF 21-APR-2000; 2000WO-US010741.  
XX  
PR 22-APR-1999; 99US-0130488P.  
XX  
PR 28-MAY-1999; 99US-0136741P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI ) UNIV MICHIGAN.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (GENT/) GENTZ R L.  
PA (DILL/) DILLON P J.  
PA (DIXI/) DIXIT V M.  
XX  
PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;  
XX  
DR WPI; 2000-687263/67.  
DR N-PSDB; AAC68777.  
XX  
XX Treating graft-versus-host disease, cancer, immunodeficiency or an  
PT autoimmune disease comprising administering an antibody to Death Domain  
PT Containing Receptor proteins and a second therapeutic agent.  
XX  
PS Claim 1; Fig 2; 273pp; English.  
XX  
CC The present invention provides the protein and coding sequences for two  
CC death domain containing receptors, designated DR3 and DR3-V1. These  
CC receptors are involved in apoptosis, and the sequences given can be used  
CC in the treatment of cancers, infections, cardiovascular disorders such as  
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms  
CC and congenital heart defects, neurodegenerative diseases including  
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple  
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,  
CC and to promote angiogenesis and wound healing  
XX  
SQ Sequence 417 AA;  
Query Match 100.0%; Score 2323; DB 3; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.3e-161;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEQRPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Db 1 MEQRPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCSSAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCSSAVADTRCGCKPG 120  
Qy 121 WFVEQVSCVSSSPFYCQPCDCLCGALHRRHRLCSRRDTCGTCPLPGFYEHGDCVSCP 180  
Db 121 WFVEQVSCVSSSPFYCQPCDCLCGALHRRHRLCSRRDTCGTCPLPGFYEHGDCVSCP 180  
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADDEAG 240  
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADDEAG 240  
Qy 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300  
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300  
Qy 301 DOLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTLGLEAE 360  
Db 301 DOLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTLGLEAE 360  
Qy 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417  
Db 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417  
RESULT 7  
AAB97370  
ID AAB97370 standard; protein; 417 AA.  
XX  
AC AAB97370;  
XX  
DT 15-AUG-2001 (first entry)  
XX  
DE Human rheumatoid arthritis associated transmembrane protein.  
XX

Rheumatoid arthritis; transmembrane protein; human.  
Homo sapiens.  
WO200132921-A2.  
XX  
PD 10-MAY-2001.  
XX  
PF 01-NOV-2000; 2000WO-JP007690.  
XX  
PR 01-NOV-1999; 99JP-00310805.  
XX  
PA (SHIO/) SHIOZAWA S.  
XX  
PI Shiozawa S, Konishi Y;  
XX  
DR WPI; 2001-308750/32.  
DR N-PSDB; AAH27782.  
XX  
PT Diagnosing rheumatoid arthritis by probing digested human genomic DNA or  
PT comparing expression of mRNA or polypeptide of a region of transmembrane  
PT protein.  
XX  
PS Disclosure; Page 15-17; 21pp; Japanese.  
XX  
CC This invention relates to a method of diagnosing chronic rheumatoid  
CC arthritis by digesting human genomic DNA with EcoRI and hybridising it  
CC with a probe for the DNA encoding the present protein which is a  
CC rheumatoid arthritis associated transmembrane protein. The method is used  
CC for the diagnosis of chronic rheumatoid arthritis, and for developing new  
CC treatments  
XX  
SQ Sequence 417 AA;  
Query Match 100.0%; Score 2323; DB 4; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.3e-161;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEQRPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Db 1 MEQRPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCSSAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCSSAVADTRCGCKPG 120  
Qy 121 WFVEQVSCVSSSPFYCQPCDCLCGALHRRHRLCSRRDTCGTCPLPGFYEHGDCVSCP 180  
Db 121 WFVEQVSCVSSSPFYCQPCDCLCGALHRRHRLCSRRDTCGTCPLPGFYEHGDCVSCP 180  
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADDEAG 240  
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADDEAG 240  
Qy 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300  
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300  
Qy 301 DOLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTLGLEAE 360  
Db 301 DOLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTLGLEAE 360  
Qy 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417  
Db 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417  
RESULT 8  
AAO17879  
ID AAO17879 standard; protein; 417 AA.  
XX  
AC AAO17879;  
XX



QY 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
DB 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120  
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120  
QY 121 WFVEQCVSQVSSSPFYCPCLDCGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180  
DB 121 WFVEQCVSQVSSSPFYCPCLDCGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180  
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADAG 240  
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADAG 240  
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLGNSWTPGYPETQEALCPQVTSW 300  
DB 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLGNSWTPGYPETQEALCPQVTSW 300  
QY 301 DQLPSRALGPAAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360  
DB 301 DQLPSRALGPAAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360  
QY 361 IEAVEVEIGRPRDQOQYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417  
DB 361 IEAVEVEIGRPRDQOQYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417

## RESULT 10

ABG73993  
ID ABG73993 standard; protein; 417 AA.

AC ABG73993;

DT 01-APR-2003 (first entry)

DE Human Apo3 protein.

XX APO-3; human; apoptosis; monoclonal antibody; cytostatic; cancer;  
KW autoimmune; inflammatory; neurodegenerative disease.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1..24  
FT /label= signal\_peptide  
FT Domain 25..198  
FT /note= "Extracellular domain"  
FT Modified-site 67  
FT /note= "N glycosylated"  
FT Modified-site 106  
FT /note= "N glycosylated"  
FT Domain 199..224  
FT /note= "Transmembrane domain"  
FT Domain 225..417  
FT /note= "Intracellular domain"  
FT Region 236  
FT /note= "This Alanine is not present in the Apo3 variant that is expressed in foetal heart"

XX US6469144-B1.

PN 22-OCT-2002.

XX 31-MAR-1997; 97US-00828683.

XX 01-APR-1996; 96US-00625328.

XX 23-SEP-1996; 96US-00710802.

PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ;

PI

XX WPI; 2003-147110/14.  
DR N-PSDB; ABX15842.  
XX Novel isolated monoclonal antibody useful for activating or stimulating  
PT apoptosis in cancer cells, comprises an antigen binding site which binds  
PT to an Apo-2 ligand inhibitor polypeptide or to an Apo-3 polypeptide.  
XX Claim 1; Fig 4; 48pp; English.

XX This invention relates to an isolated monoclonal antibody comprising an  
CC antigen binding site which binds to an Apo-2 ligand inhibitor (Apo-2LI)  
CC polypeptide and an antibody that binds the Apo3 protein. The antibodies  
CC of the invention may have cytostatic activity and may act as activators  
CC or stimulator of apoptosis in cancer cells, as blockers of excessive  
CC apoptosis or of the autoimmune/inflammatory effects of Apo-3 resulting  
CC from nuclear factor (NF)-kappaB activation or C-Jun-amino-terminal kinase  
CC (JNK) activation. The anti-Apo-2 ligand inhibitor is useful in  
CC therapeutic purposes for activating or stimulating apoptosis in cancer  
CC cells and may be used to block excessive apoptosis (for example in  
CC neurodegenerative disease), or to block potential autoimmune/  
CC inflammatory effects of Apo-3 resulting from nuclear factor (NF)-kappaB  
CC activation or C-Jun-amino-terminal kinase (JNK) activation. The antibody  
CC may also be used in diagnostic assays for Apo-2LI or Apo-3, e.g.  
CC detecting Apo-2LI or Apo-3 expression in specific cells, tissues or  
CC serum, or for affinity purification of Apo-2LI or Apo-3 from recombinant  
CC cell culture or natural sources. The present sequence represents the  
CC human Apo3 protein which was used to generate the antibody of the  
CC invention

XX Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 6; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.3e-161;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
DB 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120  
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120  
QY 121 WFVEQCVSQVSSSPFYCPCLDCGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180  
DB 121 WFVEQCVSQVSSSPFYCPCLDCGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180  
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADAG 240  
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADAG 240  
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLGNSWTPGYPETQEALCPQVTSW 300  
DB 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLGNSWTPGYPETQEALCPQVTSW 300  
QY 301 DQLPSRALGPAAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360  
DB 301 DQLPSRALGPAAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360  
QY 361 IEAVEVEIGRPRDQOQYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417  
DB 361 IEAVEVEIGRPRDQOQYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417

## RESULT 11

ABU08252  
ID ABU08252 standard; protein; 417 AA.

XX AC ABU08252;

XX DT 13-MAY-2003 (first entry)

XX



DE XX Human Apo-3 protein.

KW Human; Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; AIDS; acquired immunodeficiency syndrome; stroke; Alzheimer's disease; cancer; Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis; retinitis pigmentosa; aplastic anaemia; cerebellar degeneration; myocardial infarction; reperfusion injury; toxin-induced liver disease; chromosome 1q36.3; programmed cell death.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 1..198

FT /label= Extracellular domain

FT /note= "This domain is claimed in claim 26"

FT Domain 338..417

FT /label= Death domain

FT /note= "This domain is claimed in claim 27"

XX US2002165157-A1.

XX PD 07-NOV-2002.

XX PF 21-FEB-2002; 2002US-00081280.

XX PR 01-APR-1996; 96US-0014699P.

XX PR 23-SEP-1996; 96US-0036943P.

XX PR 31-MAR-1997; 97US-00829270.

XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi AJ;

XX DR WPI; 2003-298703/29.

XX DR N-PSDB; ABX13179.

XX FT New biologically active Apo-2LI or Apo-3 polypeptide, useful for preparing a composition for treating cancer.

XX PS Claim 22; Fig 4; 45pp; English.

XX CC The invention relates to an new isolated biologically active Apo-2LI or Apo-3 having at least 80 % sequence identity with native sequence Apo-2LI or Apo-3 appearing as ABU08251 and ABU08252. Also included are a chimaeric molecule comprising the Apo-2LI fused to a heterologous amino acid sequence; a dimer molecule comprising a first Apo-2LI and a second Apo-2LI, an antibody that binds to Apo-2LI or Apo-3 (or to its extracellular domain sequence), an isolated nucleic acid encoding Apo-2LI or Apo-3, a vector comprising the nucleic acid, a host cell comprising the vector, a method of producing Apo-2LI and a non-human (transgenic or knockout) animal that contains cells that express nucleic acid encoding Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3 are involved in apoptosis (programmed cell death) which is implicated in AIDS, (acquired immunodeficiency syndrome), stroke, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis pigmentosa, aplastic anaemia, cerebellar degeneration, myocardial infarction, reperfusion injury and toxin-induced liver disease. The gene for both proteins is located on chromosome 1q36.3 Apo-2LI and Apo-3 are also useful for preparing a composition for treating cancer. The present sequence represents Apo-3

SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 6; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.3e-161;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEQPRGCAAAVALLLVLLGARAGGTRSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARQCACDEQASQVALENCASAVADTRCGCKPG 120

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Qy 121 WFVECVSQVSSSPFFCQPCLDGALHRRHTRLLCSRDDTDCGTCLPGFYEHGDCVSCP 180

Db 121 WFVECVSQVSSSPFFCQPCLDGALHRRHTRLLCSRDDTDCGTCLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQFVVOVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADAG 240

Db 181 TSTLGSCPERCAAVCGWRQFVVOVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADAG 240

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Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWPGYPETQEALCQVTTWSW 300

Qy 301 DQLPSRALGPAAPATLSPSPAGSPANMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360

Db 301 DQLPSRALGPAAPATLSPSPAGSPANMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360

Qy 361 IEAVEVEIGRFRDQOQYEMLKRWRQCPAGLCAVVAALERMGLDCGVEDLRSRLQGP 417

Db 361 IEAVEVEIGRFRDQOQYEMLKRWRQCPAGLCAVVAALERMGLDCGVEDLRSRLQGP 417

RESULT 12

ABG73859

ID ABG73859 standard; protein; 417 AA.

XX AC ABG73859;

XX DT 03-APR-2003 (first entry)

XX DE Human foetal heart Apo-3 protein.

XX KW Human; Apo-3; apoptosis; induce apoptosis; inhibit apoptosis; TNFR; nuclear factor-kappa B; NF-kappa B; Alzheimer's disease; AIDS; tumour necrosis factor receptor; acquired immunodeficiency syndrome; Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis; retinitis pigmentosa; cerebellar degeneration; aplastic anaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; cancer; lupus; herpes virus infection.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 1..198

FT /note= "Extracellular domain. This domain is specifically claimed in claim 2 of the specification"

FT Peptide 1..24

FT Protein 25..417

FT /label= Signal peptide

FT /note= "Mature Apo-3 protein"

FT Modified-site 67

FT /note= "N-glycosylated"

FT Modified-site 106

FT /note= "N-glycosylated"

FT Domain 199..224

FT /note= "Transmembrane domain"

FT Domain 225..417

FT /note= "Intracellular domain"

FT Domain 338..417

FT /note= "Death domain. This domain is specifically claimed in claim 3 of the specification"

XX PN US6462176-B1.

XX PD 08-OCT-2002.

XX PF 11-SEP-1997; 97US-00928069.

XX PR 23-SEP-1996; 96US-0026943P.

XX PA (GETH ) GENENTECH INC.







**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2005, 13:40:47 ; Search time 161 Seconds  
(without alignments)  
996.003 Million cell updates/sec

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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2323	100.0	417	9	US-09-333-966-4
2	2323	100.0	417	9	US-09-874-138-5
3	2323	100.0	417	9	US-09-993-234-6
4	2323	100.0	417	10	US-09-314-889-4
5	2323	100.0	417	13	US-10-005-842-5
6	2323	100.0	417	13	US-10-081-280-6
7	2323	100.0	417	13	US-10-112-793-6
8	2323	100.0	417	14	US-10-112-193-10
9	2323	100.0	417	14	US-10-175-902-5
10	2323	100.0	417	14	US-10-189-189-4
11	2323	100.0	417	14	US-10-210-951-24

12	2323	100.0	417	14	US-10-211-884-24
13	2323	100.0	417	14	US-10-310-793-4
14	2323	100.0	417	15	US-10-211-858-24
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17	2323	100.0	417	16	US-10-774-622-5
18	2323	100.0	417	16	US-10-744-379-2
19	2323	100.0	833	14	US-10-226-296-5
20	2323	100.0	833	14	US-10-226-318-5
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24	2267	97.6	428	10	US-09-314-889-2
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29	1051	45.2	181	13	US-10-081-280-1
30	1051	45.2	181	13	US-10-112-793-1
31	1051	45.2	181	14	US-10-112-193-1
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ALIGNMENTS

RESULT 1  
US-09-333-966-4  
; Sequence 4, Application US/09333966  
; Patent No. US20020009773A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/333,966  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,469  
; FILING DATE:  
; APPLICATION NUMBER: No. US20020009773A1 Yet Assigned  
; FILING DATE: 06-FEB-1997  
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-333-966-4

Query Match 100.0%; Score 2323; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-874-138-5
; Sequence 5, Application US/09874138
; Patent No. US2002072091A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Yu, Guo-liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.1310006
; CURRENT APPLICATION NUMBER: US/09/874,138
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/565,009
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/148,939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133,238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132,498
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; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042,583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054,021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040,846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-138-5

Query Match 100.0%; Score 2323; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
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QY 301 DQPSRALGPAAPTLPSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
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RESULT 3
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; Sequence 6, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
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; FILING DATE: 19-No. US20020146768A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/828,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino acid
; TOPOLOGY: Linear
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US-09-993-234-6

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Best Local Similarity 100.0%; Pred. No. 5.3e-163;
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DB 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60

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QY 361 IEAVEVEIGRFDQOQYEMLKRWROQOPAGLGA VAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFDQOQYEMLKRWROQOPAGLGA VAAALERMGLDGCVEDLRSRLQRP 417

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## RESULT 4

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; Sequence 4, Application US/09314889
; Publication No. US20030077694A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/314,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/815,469
; FILING DATE:
; APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-314-889-4

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Query Match 100.0%; Score 2323; DB 10; Length 417;

Best Local Similarity 100.0%; Pred. No. 5.3e-163;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCSSAVADTRCGCKPG 120

QY 121 WFVEQVSCQVSSSPFYCPQCLDCGALHRRTRLLCSRRTDCGTCPLPGFYEHGDCVSCP 180
DB 121 WFVEQVSCQVSSSPFYCPQCLDCGALHRRTRLLCSRRTDCGTCPLPGFYEHGDCVSCP 180

QY 181 TSTLGSCPERCAACVGRQMFVQVLLAGLVVPLLLGATLTYTTRHCPHPKPLVTADGAG 240
DB 181 TSTLGSCPERCAACVGRQMFVQVLLAGLVVPLLLGATLTYTTRHCPHPKPLVTADGAG 240

QY 241 MEALTPPPATHLSPLDSAHTLLAPDSSEKICTVOLVGNSTWTPGYPTQEALCPQVTSW 300
DB 241 MEALTPPPATHLSPLDSAHTLLAPDSSEKICTVOLVGNSTWTPGYPTQEALCPQVTSW 300

QY 301 DQPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
DB 301 DQPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360

QY 361 IEAVEVEIGRFDQOQYEMLKRWROQOPAGLGA VAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFDQOQYEMLKRWROQOPAGLGA VAAALERMGLDGCVEDLRSRLQRP 417

```

## RESULT 5

```

; Sequence 5, Application US/10005842
; Publication No. US20020098550A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Su, Jeffrey
; APPLICANT: Rosen, Craig A.

```

;; TITLE OF INVENTION: Death Domain Containing Receptor 5  
;; NUMBER OF SEQUENCES: 12  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Human Genome Sciences, Inc.  
;; STREET: 9410 Kelly West Avenue  
;; CITY: Rockville  
;; STATE: MD  
;; COUNTRY: US  
;; ZIP: 20850  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/005,842  
;; FILING DATE: 07-Dec-2001  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/042,583  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: US 60/040,846  
;; FILING DATE: 17-MAR-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hoover, Kenley  
;; REGISTRATION NUMBER: 40,302  
;; REFERENCE/DOCKET NUMBER: PF366  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 3013098504  
;; TELEFAX: 3013098439  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 417 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-005-842-5

Query Match 100.0%; Score 2323; DB 13; Length 417;  
Best Local Similarity 100.0%; Pred. No. 5.3e-163;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEQRPRGCAAAVAAALLLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Db 1 MEQRPRGCAAAVAAALLLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Qy 121 WFVECVSQVSSSPFFYCPCLDCGALHRHTRLLCSRRTDCGCLPGFYEHGDCVSCP 180  
Db 121 WFVECVSQVSSSPFFYCPCLDCGALHRHTRLLCSRRTDCGCLPGFYEHGDCVSCP 180  
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD EAG 240  
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD EAG 240  
Qy 241 MEALTTPPPATHSLPDSAHILLAPPDSSEKICTVOLVGNSTWTPGYPTQEQALCPQVTWSW 300  
Db 241 MEALTTPPPATHSLPDSAHILLAPPDSSEKICTVOLVGNSTWTPGYPTQEQALCPQVTWSW 300  
Qy 301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTILGLREAE 360  
Db 301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTILGLREAE 360  
Qy 361 IEAVEVEIGRFDOQYEMLKWROQQPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417  
Db 361 IEAVEVEIGRFDOQYEMLKWROQQPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417

RESULT 6  
US-10-081-280-6  
; Sequence 6, Application US/10081280  
; Publication No. US20020185157A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/081,280  
; FILING DATE: 21-Feb-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/829,270  
; FILING DATE: 31-Mar-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1007R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5416  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: Amino acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-081-280-6

Query Match 100.0%; Score 2323; DB 13; Length 417;  
Best Local Similarity 100.0%; Pred. No. 5.3e-163;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEQRPRGCAAAVAAALLLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Db 1 MEQRPRGCAAAVAAALLLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Qy 121 WFVECVSQVSSSPFFYCPCLDCGALHRHTRLLCSRRTDCGCLPGFYEHGDCVSCP 180  
Db 121 WFVECVSQVSSSPFFYCPCLDCGALHRHTRLLCSRRTDCGCLPGFYEHGDCVSCP 180  
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD EAG 240  
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD EAG 240  
Qy 241 MEALTTPPPATHSLPDSAHILLAPPDSSEKICTVOLVGNSTWTPGYPTQEQALCPQVTWSW 300  
Db 241 MEALTTPPPATHSLPDSAHILLAPPDSSEKICTVOLVGNSTWTPGYPTQEQALCPQVTWSW 300  
Qy 301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTILGLREAE 360  
Db 301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTILGLREAE 360  
Qy 361 IEAVEVEIGRFDOQYEMLKWROQQPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417  
Db 361 IEAVEVEIGRFDOQYEMLKWROQQPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417

Db 361 IEAVEVEIGRFDQOYEMLKRWROQOPAGLGA VYAAALERMGLDGCVEDLRSRLORGP 417

US-10-112-793-6

RESULT 7

US-10-112-793-6

Sequence 6, Application US/10112793

Publication No. US20020192729A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,793

FILING DATE: 28-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/828,683A

FILING DATE: 31-Mar-1997

APPLICATION NUMBER: 08/625328

FILING DATE: 1-Apr-1996

APPLICATION NUMBER: 08/710802

FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 417 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-112-793-6

Query Match 100.0%; Score 2323; DB 13; Length 417;

Best Local Similarity 100.0%; Pred. No. 5.3e-163;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Db 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120

Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVECVQSVSSSPFFYCPCLDCGALHRRHRLLCSSRDTCGTCPLPGFYEHGDCVSCP 180

Db 121 WFVECVQSVSSSPFFYCPCLDCGALHRRHRLLCSSRDTCGTCPLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCHWPHKPLVTADAG 240

Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCHWPHKPLVTADAG 240

Qy 241 MEALTPTTATHLSPLDLSAHTLLAPDSEKICTVOLVGNWSWTPGYPETQEALCPQVTSW 300

Db 241 MEALTPTTATHLSPLDLSAHTLLAPDSEKICTVOLVGNWSWTPGYPETQEALCPQVTSW 300

Qy 301 DQLPSRALGPAAAPTSLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360

Db 301 DQLPSRALGPAAAPTSLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360

Qy 361 IEAVEVEIGRFDQOYEMLKRWROQOPAGLGA VYAAALERMGLDGCVEDLRSRLORGP 417

Db 361 IEAVEVEIGRFDQOYEMLKRWROQOPAGLGA VYAAALERMGLDGCVEDLRSRLORGP 417

RESULT 8

US-10-112-193-10

Sequence 10, Application US/10112193

Publication No. US20030004313A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-3 POLYPEPTIDE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,193

FILING DATE: 28-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/928,069

FILING DATE: 11-Sep-1997

APPLICATION NUMBER: 60/026943

FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1052R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 417 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-10-112-193-10

Query Match 100.0%; Score 2323; DB 14; Length 417;

Best Local Similarity 100.0%; Pred. No. 5.3e-163;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Db 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120

Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVECVQSVSSSPFFYCPCLDCGALHRRHRLLCSSRDTCGTCPLPGFYEHGDCVSCP 180

Db 121 WFVECVQSVSSSPFFYCPCLDCGALHRRHRLLCSSRDTCGTCPLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCHWPHKPLVTADAG 240

Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCHWPHKPLVTADAG 240

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Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNWTPGYPETQEALCPQVWTSW 300
Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNWTPGYPETQEALCPQVWTSW 300
Qy 301 DQLPSRALGPAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db 301 DQLPSRALGPAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Qy 361 IEAVEVEIGRDOOQYEMLKRWROQOPAGLCAVVAALERMGLDCGVEDLRSRLQGP 417
Db 361 IEAVEVEIGRDOOQYEMLKRWROQOPAGLCAVVAALERMGLDCGVEDLRSRLQGP 417

RESULT 9
US-10-175-902-5
; Sequence 5, Application US/10175902
; Publication No. US20030108516A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.130005
; CURRENT APPLICATION NUMBER: US/10175,902
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-175-902-5

Query Match 100.0%; Score 2323; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCAQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCAQACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSVQCVSSSPFFCQPCDCLCGALHRRHRLILCSRRTDCGTCLPGFYEHGDCVSCP 180
Db 121 WFVECVQSVQCVSSSPFFCQPCDCLCGALHRRHRLILCSRRTDCGTCLPGFYEHGDCVSCP 180
Qy 181 TSTLGSQPCERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD EAG 240
Db 181 TSTLGSQPCERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD EAG 240
Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNWTPGYPETQEALCPQVWTSW 300
Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNWTPGYPETQEALCPQVWTSW 300
Qy 301 DQLPSRALGPAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db 301 DQLPSRALGPAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
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Qy 361 IEAVEVEIGRDOOQYEMLKRWROQOPAGLCAVVAALERMGLDCGVEDLRSRLQGP 417
Db 361 IEAVEVEIGRDOOQYEMLKRWROQOPAGLCAVVAALERMGLDCGVEDLRSRLQGP 417

RESULT 10
US-10-189-189-4
; Sequence 4, Application US/10189189
; Publication No. US20030170203A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; FILE REFERENCE: 1488.031000C
; CURRENT APPLICATION NUMBER: US/10189,189
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: US 60/314,314
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/303,155
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 09/557,908
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: US 60/136,741
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 60/130,488
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 08/815,469
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: US 60/037,341
; PRIOR FILING DATE: 1997-02-06
; PRIOR APPLICATION NUMBER: US 60/028,711
; PRIOR FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/013,285
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-189-4

Query Match 100.0%; Score 2323; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCAQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCAQACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSVQCVSSSPFFCQPCDCLCGALHRRHRLILCSRRTDCGTCLPGFYEHGDCVSCP 180
Db 121 WFVECVQSVQCVSSSPFFCQPCDCLCGALHRRHRLILCSRRTDCGTCLPGFYEHGDCVSCP 180
Qy 181 TSTLGSQPCERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD EAG 240
Db 181 TSTLGSQPCERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD EAG 240
Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNWTPGYPETQEALCPQVWTSW 300
Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNWTPGYPETQEALCPQVWTSW 300
Qy 301 DQLPSRALGPAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db 301 DQLPSRALGPAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
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Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Qy 121 WFEVCQVSSQVSSPFYQCPCLDCGALHRRHRLTCSRRTDCGTCCLPGFVEHGDGCVSCP 180  
Db 121 WFEVCQVSSQVSSPFYQCPCLDCGALHRRHRLTCSRRTDCGTCCLPGFVEHGDGCVSCP 180  
Qy 181 TSTLGSQVSSQVSSPFYQCPCLDCGALHRRHRLTCSRRTDCGTCCLPGFVEHGDGCVSCP 240  
Db 181 TSTLGSQVSSQVSSPFYQCPCLDCGALHRRHRLTCSRRTDCGTCCLPGFVEHGDGCVSCP 240  
Qy 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPETQALCPQVTSW 300  
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPETQALCPQVTSW 300  
Qy 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPQPOLYDMDAVPARRWKEFVRTLGLREAE 360  
Db 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPQPOLYDMDAVPARRWKEFVRTLGLREAE 360  
Qy 361 IEAVEVEIGRDOQYEMLKWROQOQAGLVAVYAAALERMGLDGCVEDLSRLQRP 417  
Db 361 IEAVEVEIGRDOQYEMLKWROQOQAGLVAVYAAALERMGLDGCVEDLSRLQRP 417  
RESULT 13  
US-10-310-793-4  
; Sequence 4, Application US/10310793  
; Publication No. US20030198640A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Zhang, Jun  
; APPLICANT: Wei, Ping  
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases  
; FILE REFERENCE: PF573  
; CURRENT APPLICATION NUMBER: US/10/310,793  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR FILING DATE: 2002-08-23  
; PRIOR FILING DATE: 2002-08-23  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR FILING DATE: 1999-05-13  
; PRIOR FILING DATE: 1999-05-13  
; PRIOR FILING DATE: 1999-05-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: human  
US-10-310-793-4  
Query Match 100.0%; Score 2323; DB 14; Length 417;  
Best Local Similarity 100.0%; Pred. No. 5.3e-163;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEORPRCAAAVALLLVLLGARAQGTSPRCDACDGHKKIGLFCRCGPCAGHYLKAP 60  
Db 1 MEORPRCAAAVALLLVLLGARAQGTSPRCDACDGHKKIGLFCRCGPCAGHYLKAP 60  
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120  
Qy 121 WFEVCQVSSQVSSPFYQCPCLDCGALHRRHRLTCSRRTDCGTCCLPGFVEHGDGCVSCP 180  
Db 121 WFEVCQVSSQVSSPFYQCPCLDCGALHRRHRLTCSRRTDCGTCCLPGFVEHGDGCVSCP 180  
Qy 181 TSTLGSQVSSQVSSPFYQCPCLDCGALHRRHRLTCSRRTDCGTCCLPGFVEHGDGCVSCP 240  
Db 181 TSTLGSQVSSQVSSPFYQCPCLDCGALHRRHRLTCSRRTDCGTCCLPGFVEHGDGCVSCP 240  
Qy 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPETQALCPQVTSW 300  
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPETQALCPQVTSW 300  
Qy 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPQPOLYDMDAVPARRWKEFVRTLGLREAE 360  
Db 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPQPOLYDMDAVPARRWKEFVRTLGLREAE 360  
Qy 361 IEAVEVEIGRDOQYEMLKWROQOQAGLVAVYAAALERMGLDGCVEDLSRLQRP 417  
Db 361 IEAVEVEIGRDOQYEMLKWROQOQAGLVAVYAAALERMGLDGCVEDLSRLQRP 417  
RESULT 14  
US-10-211-858-24  
; Sequence 24, Application US/10211858  
; Publication No. US20030211096A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Marsters, Scot A.  
; APPLICANT: Pan, James  
; APPLICANT: Pitti, Robert M.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stone, Donna M.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR  
; FILE REFERENCE: P2931R1C1  
; CURRENT APPLICATION NUMBER: US/10/211,858  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR FILING DATE: 1996-04-01  
; PRIOR FILING DATE: 1996-04-01  
; PRIOR FILING DATE: 1996-09-23  
; PRIOR FILING DATE: 1996-09-23  
; PRIOR FILING DATE: 1997-07-17  
; PRIOR FILING DATE: 1997-07-17  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR FILING DATE: 1997-11-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 258

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; SEQ ID NO 24
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-858-24

Query Match      100.0%; Score 2323; DB 15; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQRPRGCAAVAAALLVLLGARAQGGTRSPRCDACGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAAVAAALLVLLGARAQGGTRSPRCDACGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDITFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDITFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVECOVSQCYSVSSPFYQPCDCLDCGALHHRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
Db 121 WFVECOVSQCYSVSSPFYQPCDCLDCGALHHRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADEAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADEAG 240

Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNWSWTPGYPETQEALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNWSWTPGYPETQEALCPQVTWSW 300

Qy 301 DOLPSRALGPAAPATLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTTLGLREAE 360
Db 301 DOLPSRALGPAAPATLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTTLGLREAE 360

Qy 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAANYAALERMGLDGCVEDLRSRLQGP 417
Db 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAANYAALERMGLDGCVEDLRSRLQGP 417

RESULT 15
US-10-415-247-3
; Sequence 3, Application US/10415247
; Publication No. US20040013655A1
; GENERAL INFORMATION:
; APPLICANT: Shiozawa, Shunichi
; TITLE OF INVENTION: Genome responsible for chronic rheumatoid arthritis,
; TITLE OF INVENTION: diagnostic method, pathogenicity judging method and
; TITLE OF INVENTION: detection-use diagnostic kit of chronic rheumatoid
; TITLE OF INVENTION: arthritis, and therapeutic method and medicine of
; TITLE OF INVENTION: chronic rheumatoid arthritis
; FILE REFERENCE: TLOPI-2
; CURRENT APPLICATION NUMBER: US/10/415,247
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: JP 2000-324296
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: JP 2001-90546
; PRIOR FILING DATE: 2001-3-27
; PRIOR APPLICATION NUMBER: JP 2001-99990
; PRIOR FILING DATE: 2001-3-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-247-3

Query Match      100.0%; Score 2323; DB 15; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQRPRGCAAVAAALLVLLGARAQGGTRSPRCDACGDFHKKIGLFCRCGCPAGHYLKAP 60
```

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Db 1 MEQRPRGCAAVAAALLVLLGARAQGGTRSPRCDACGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDITFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDITFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECOVSQCYSVSSPFYQPCDCLDCGALHHRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
Db 121 WFVECOVSQCYSVSSPFYQPCDCLDCGALHHRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADEAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADEAG 240
Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNWSWTPGYPETQEALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNWSWTPGYPETQEALCPQVTWSW 300
Qy 301 DOLPSRALGPAAPATLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTTLGLREAE 360
Db 301 DOLPSRALGPAAPATLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTTLGLREAE 360
Qy 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAANYAALERMGLDGCVEDLRSRLQGP 417
Db 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAANYAALERMGLDGCVEDLRSRLQGP 417

Search completed: June 27, 2005, 13:56:23
Job time : 163 secs
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Query Match      8.5%; Score 96; DB 2; Length 149;
Best Local Similarity 33.3%; Pred. No. 1.9;
Matches 18: Conservative 7; Mismatches 29; Indels 0; Gaps 0;
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Qy .  
179 CPTSTLGSPERCAVC 195  
Db  
130 C-----GGCGSGCGSSC 141



Db 29 MRSRGRGFQVSSSLPDIYRC-GESEHLAKDCDLQED-----ACYNCGRGGHIAD 79  
QY 61 CTEP-----CGNSTCLVCPDPTFLAWENHNSECARCOACDEQASQVALENCNSAVADTR 114  
Db 80 CKEPKREEQ-----CYNCGKPGHLARDCHDADE-QKCYSCGEFGH--IQDCTKVKCYR 132  
QY 115 CGCKPGFWFVEQVQSCVSSPPYQPCLDGALHR 149  
Db 133 CG-ETGHV-----AINCSTSEVNCYRCGESGHLAR 162

## RESULT 14

I48297  
cellular nucleic acid binding protein clone 6 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I48297; S19861; S19959  
R:Warden, C.H.; Krisans, S.K.; Furcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; T  
Genomics 24, 14-19, 1994  
A:Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identif  
A:Reference number: A55499; MUID:95203870; PMID:7896269  
A:Accession: I48297  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-170 <RES>  
A:Cross-references: UNIPROT:P53996; EMBL:Z11870; NID:g50472; PIDN:CAA77896.1; PID:g50473  
R:Warden, C.H.  
submitted to the EMBL Data Library, January 1992  
A:Description: Cellular nucleic acid binding protein (CNBP) is an extremely conserved cy  
A:Reference number: S19861  
A:Accession: S19861  
A:Molecule type: mRNA  
A:Residues: 1-170 <W2>  
A:Cross-references: EMBL:X63866; NID:g50470; PIDN:CAA5345.1; PID:g50471  
C:Superfamily: cellular nucleic acid-binding protein

Query Match 7.9%; Score 89.5; DB 2; Length 170;  
Best Local Similarity 25.2%; Pred. No. 6.2;  
Matches 39; Conservative 18; Mismatches 71; Indels 27; Gaps 8;

QY 1 MEQPRGCAANVAALLVLLNAGRAQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Db 29 MRSRGRGFQVSSSLPDIYRC-GESEHLAKDCDLQED-----ACYNCGRGGHIAD 79  
QY 61 CTEP-----CGNSTCLVCPDPTFLAWENHNSECARCOACDEQASQVALENCNSAVADTR 114  
Db 80 CKEPKREEQ-----CYNCGKPGHLARDCHDADE-QKCYSCGEFGH--IQDCTKVKCYR 132  
QY 115 CGCKPGFWFVEQVQSCVSSPPYQPCLDGALHR 149  
Db 133 CG-ETGHV-----AINCSTSEVNCYRCGESGHLAR 162

## RESULT 15

I46412  
keratin KAP5.4 - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I46412; S34215  
R:Jenkins, B.J.; Powell, B.C.  
J. Invest. Dermatol. 103, 310-317, 1994  
A:Title: Differential expression of genes encoding a cysteine-rich keratin family in the  
A:Reference number: I46412; MUID:94358466; PMID:7521375  
A:Accession: I46412  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-191 <JEN>  
A:Cross-references: UNIPROT:Q28583; EMBL:X73434; NID:g313719; PIDN:CAA51829.1; PID:g3137  
C:Genetics:  
A:Gene: KRTAP5.4  
C:Superfamily: ultra-high-sulfur keratin

Query Match 7.9%; Score 89.5; DB 2; Length 191;  
Best Local Similarity 22.3%; Pred. No. 6.7;  
Matches 42; Conservative 8; Mismatches 61; Indels 77; Gaps 13;  
QY 21 GARAQGGTSPRCDCAGDFHKKIGLFCRG-----CPAGHYLKAPCTEPCGHST--CL 71  
Db 63 GCSSCGSGSKGSCGCGG-----CGSSCCCKPVCCCVPCVSCSSCGGCGGSGGSGGCGG 117  
QY 72 VCPQDTFLAWENHNSECARCOACDEQASQVALENCNSAVADTRCGCKPGFWFVEQVQSCV 131  
Db 118 SC-----GGSKGCGSGCGGSG-----GGCP-----SCCVPVCC 146  
QY 132 SSSPFYQPCLDGALHRTLLCSRRTDCGTCLPGFYEHGDC--VSC--PTSTLQSC 187  
Db 147 -----CVPACSCSS-----CGK--GGCGSC-----GCSQSSCCRPCCSQSSC 181  
QY 188 PERCAAVC 195  
Db 182 ---CVPVC 186

Search completed: June 27, 2005, 14:02:57  
Job time : 44 secs

**100% WHITE BLANK (USPTO)**



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2005, 13:43:43 ; Search time 171 Seconds  
(without alignments)

583.950 Million cell updates/sec

Title: US-10-081-280-6\_COPY\_1\_195

Perfect score: 1130

Sequence: 1 MEQRPRCAVAALLLVLL.....CVSPTSTLSCPERCAAVC 195

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 635772

Minimum DB seq length: 0

Maximum DB seq length: 195

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	17.5	189	2 Q95185	Q95185 felis silve
2	197	17.4	189	2 Q97530	Q97530 canis famil
3	173	15.3	150	2 Q9R230	Q9R230 rattus norv
4	164.5	14.6	176	1 TR23 MOUSE	Q9er63 mus musculu
5	161.5	14.3	130	2 Q9WJ70	Q9mj20 macaca mula
6	157.5	13.9	186	2 Q911R5	Q911r5 vaccinia vi
7	157.5	13.9	186	2 Q9WJB4	Q9wjB4 vaccinia vi
8	155	13.7	186	2 Q97235	Q97235 cowpox viru
9	153.5	13.6	186	2 Q9YP87	Q9yp87 cowpox viru
10	146.5	13.0	146	2 Q9Z2V4	Q9zzy4 gallus gall
11	137.5	12.2	169	2 Q9TKE0	Q9jke0 rattus norv
12	135.5	11.8	124	2 Q8SQS1	Q8sqS1 felis silve
13	133.5	11.8	147	2 Q8SQS2	Q8sqS2 felis silve
14	132	11.7	117	2 Q6VZR1	Q6vzr1 canarypox v
15	128	11.3	176	2 Q9PZS2	Q9pzs2 human cytom
16	126.5	11.2	65	2 Q8SQ49	Q8sq49 felis silve
17	125	11.1	110	2 Q9BIR2	Q9bir2 paramecium
18	124	11.0	110	2 Q9BIR3	Q9bir3 paramecium
19	123	10.9	167	2 Q8BDC5	Q8bdc5 human cytom
20	123	10.9	176	2 Q911R3	Q911r3 human cytom
21	123	10.9	176	2 Q9PZS1	Q9pzs1 human cytom
22	123	10.9	176	2 Q9PZS3	Q9pzs3 human cytom
23	122	10.8	176	2 Q910W9	Q910w9 human cytom
24	122	10.8	176	2 Q911R4	Q911r4 human cytom
25	122	10.8	176	2 Q9PZS5	Q9pzs5 human cytom
26	121.5	10.8	172	2 Q911R0	Q911r0 human cytom
27	119	10.5	151	2 Q6P2H9	Q6p2h9 homo sapien
28	115	10.2	175	2 Q9PZR6	Q9pzs6 human cytom
29	114	10.1	194	2 Q7PI78	Q7pi78 anopheles g
30	113.5	10.0	175	2 Q9PZS5	Q9pzs5 human cytom
31	113	10.0	195	2 Q9D141	Q9d141 mus musculu

32	112	9.9	175	2 Q9PWX3	Q9pwx3 human cytom
33	112	9.9	175	2 Q9PZS8	Q9pzs8 human cytom
34	111.5	9.9	166	2 Q8BDC6	Q8bdc6 human cytom
35	111.5	9.9	175	2 Q910H9	Q910h9 human cytom
36	111.5	9.9	175	2 Q6SWR4	Q6swr4 human cytom
37	111.5	9.9	175	2 Q6SWX0	Q6swx0 human cytom
38	111.5	9.9	175	2 Q9PWY0	Q9pwy0 human cytom
39	111.5	9.9	175	2 Q9PX94	Q9px94 human cytom
40	111.5	9.9	175	2 Q9PXA1	Q9pxa1 human cytom
41	111.5	9.9	175	2 Q9PZR0	Q9pzs0 human cytom
42	111.5	9.9	175	2 Q9PZR4	Q9pzs4 human cytom
43	111.5	9.9	175	2 Q9PZR7	Q9pzs7 human cytom
44	111.5	9.9	175	2 Q9PZS6	Q9pzs6 human cytom
45	111.5	9.9	175	2 Q9PZS7	Q9pzs7 human cytom

ALIGNMENTS

RESULT 1  
Q95185 PRELIMINARY; PRT; 189 AA.  
AC Q95185;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Tumour necrosis factor receptor p60 (Fragment).  
GN Name=TNFR-1;  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OC NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Duthie S., Nasir L., Eckersall P.D.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U72344; AAB95089.1; -;  
DR HSSP; P19438; 1EXT.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR000345; CytC\_heme\_BS.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
KW Receptor.  
FT NON TER 189  
SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;

Query Match 17.5%; Score 198; DB 2; Length 189;

Best Local Similarity 29.4%; Pred. No. 5.3e-09;

Matches 52; Conservative 19; Mismatches 90; Indels 16; Gaps 4;

Qy	11	VAAALLLVLLGARAQG-----GTRSPRCAGDFHKKIGLFCRCGCPAGHYLKAPCT 62
Db	14	VLLALLVEIYPLRVTLGLVPLHLDREKRAIPCQGGYIHPQDNSICCTCKHGTYLNDCE 73
Qy	63	BPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCSAVADTRCGCKPGWF 122
Db	74	GPGLDTDCRENGTFTASENYLR-QCLSCSKCKEMYQVEISPTVYRDVCGCRKN-- 130
Qy	123	VECVSQSVSSPFVCPCLDCGALHRRTRLLCRRDTCGTCPLPGFVHEHGDGVCVC 179
Db	131	---QRYWSETHFOCLNCSLC--LNGTVQISCKETQNTVCTCHAGFFLRNECVSC 182

RESULT 2

Q97530 PRELIMINARY; PRT; 189 AA.

ID Q97530

AC Q97530;

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DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Tumor necrosis factor receptor p50 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21109092; PubMed=1182158; DOI=10.1016/S0165-2427(00)00261-0;
RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S.,
RA Bennett D.;
RT "Cloning of canine IL-1ra, TNFR and TIMP-2.";
RL Vet. Immunol. Immunopathol. 78:207-214(2001).
DR EMBL; AF013955; AAD01516.1; -.
DR HSSP; P19438; 1TNR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR00345; CytC_heme_BS.
DR InterPro; IPR005209; EGF_Like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON TER 189
SQ SEQUENCE 189 AA; 21324 MW; 5D3AD6A5676BFE99 CRC64;

Query Match 17.4%; Score 197; DB 2; Length 189;
Best Local Similarity 28.6%; Pred. No. 6.5e-09;
Matches 52; Conservative 17; Mismatches 87; Indels 26; Gaps 5;

Qy 11 VAAALLVLLGARAQGGTTRSPR-----CDCAGDFHKIKGLFCRCGCPAGHYLKAPCT 62
Db 14 VLLALLEIPISVTALVPHPRNVRKAILCPQGYIHPQDDSICTCKHGTYLYNDGP 73
Qy 63 EPCGNSTCLVCPQDTFLAWNHNSCARCOACDEQASQVALENCNSAVADTRCGKPG-- 120
Db 74 GPGLDTCRECENGTFTASENHLR-QCLSCSKCKEMNQVEISPTVYRDTVCGRKNQY 132
Qy 121 ---WFVECVQSVSSPFYQCPCLDCGALHRHRLCSRDTCGCLPGFYEHGDGV 177
Db 133 RFYW-----SETLFQCNCSLC--LNGTVQISQCEKQNTICTCHAGFFLREHECV 180
Qy 178 SC 179
Db 181 SC 182

RESULT 3
ID Q9R230 PRELIMINARY; PRT; 150 AA.
AC Q9R230;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Fas receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Corpus luteum;
RA Lareu R.R., Dharmarajan A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104034; AAD2021.1; -.
DR HSSP; O92956; 1JMA.
DR GO; GO:0016020; C:membrane; IEA.
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DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 150
SQ SEQUENCE 150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;

Query Match 15.3%; Score 173; DB 2; Length 150;
Best Local Similarity 28.9%; Pred. No. 5.5e-07;
Matches 43; Conservative 16; Mismatches 66; Indels 24; Gaps 5;

Qy 13 AALLLVLLG-----ARAQG-----GTRSPRCDGDFHKIKGLFCRCGCPAGHY 56
Db 1 AVLPLVLAPGLNVRMQGTDISISGLKRSVRETDNNCSGLY-QVGPFCQCPQGER 59
Qy 57 LKAPCTEPCGNSTCLVCPQDTFLAWNHNSCARCOACDEQASQVALENCNSAVADTRCG 116
Db 60 KVXDCTTSGGAPTCHEEYTDKHYSDKRCACFACDEGHGCGLEVTNCTRTQNTYKCR 119
Qy 117 CKPGWFVECVQSVSSPFYQCPCLDCG 145
Db 120 CKENFY--CNASLC-----DHCYHCTSCG 141

RESULT 4
TR23 MOUSE
ID TR23 MOUSE STANDARD; PRT; 176 AA.
AC Q9ER63; Q8VHC0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 23 precursor (Tumor
DE necrosis factor receptor p60 homolog 1) (TNF receptor family member
DE SOB) (Decoy TRAIL receptor 1) (TNF receptor homolog 1).
DE GN Name=Tnfrsf23; Synonyms=Dctrailr1, Tnfrh1, Tnfrsf1a1;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv; TISSUE=Embryonic stem cells;
RX MEDLINE=20519229; PubMed=11063728; DOI=10.1093/hmg/9.18.2691;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region;
RT implications for a novel imprinting centre and extended imprinting.";
RL Hum. Mol. Genet. 9:2691-2706(2000).
RN [2]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND 3D-STRUCTURE
RC MODELING OF 52-160.
RC STRAIN=C57BL/6;
RX PubMed=12466268; DOI=10.1074/jbc.M210783200;
RA Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A.,
RA Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M.,
RA Burkly L.C., Tschopp J., Zheng T.S.;
RT "Identification of a new murine tumor necrosis factor receptor locus
RT that contains two novel murine receptors for tumor necrosis factor-
RL related apoptosis-inducing ligand (TRAIL).";
RN J. Biol. Chem. 278:5444-5454(2003).
RN [3]
RP SEQUENCE FROM N.A.
RP Pan G., Mao W., Rissler P.;
RT "Characterization of SOB, a member of the TNFR family.";
```

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC	Cercopithecinae; Macaca.
OX	NCBI_TaxID=9544;
RN	[1]
RX	SEQUENCE FROM N.A.
RP	Petit F., Arnould D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA	Monceaux V., Ho Trong Fang R., Hurtrel B., Ameisen J.-C.,
RA	Estaque J.
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF530075; AAM95635.1; -
DR	HSSP; O14763; 1DU3.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR	GO; GO:0006915; P:apoptosis; IEA.
DR	GO; GO:0006955; P:immune response; IEA.
DR	GO; GO:0007165; P:signal transduction; IEA.
DR	InterPro; IPR008063; Fas receptor.
DR	InterPro; IPR001388; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 2.
DR	PRINTS; PR01680; FASRECEPTOR.
DR	SMART; SM00208; TNFR; 2.
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR	PROSITE; PS00500; TNFR_NGFR_2; 2.
KW	Receptor.
FT	NON_TER
FT	NON_TER
FT	NON_TER
SEQ	SEQUENCE 130 AA; 14814 MW; 91542C61323F3C27 CRC64;
	Query Match 14.3%; Score 161.5; DB 2; Length 130;
	Best Local Similarity 31.7%; Pred.No. 4.5e-06;
	Matches 32; Conservative 12; Mismatches 50; Indels 7; Gaps 1;
QY	44 GLPCCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQAQVA 103
DB	22 GQFCRNPPGGERKARDCTWNEPPCVQCQEKEYTDKGHPGSKRCRCLCDGHGLEV 81
QY	104 LENCSAVADTRCCKPGWFVEVCQVSQCVSSSPYCQPLDC 144
DB	82 EINCTRTQTKCRCKDNFF-----CNSAVCEHCDCPTKC 115
RESULT 6	
Q911R5	PRELIMINARY; PRT; 186 AA.
ID	Q911R5 AC Q911R5; 19, Created)
AC	Q911R5; 19, Last sequence update)
DT	01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DT	01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DT	01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE	Tumour necrosis family receptor.
GN	Name=A53R;
OS	Vaccinia virus.
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC	Orthopoxvirus.
OX	NCBI_TaxID=10245;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=USSR;
RC	MEDLINE=21874859; PubMed=11878931; DOI=10.1006/viro.2001.1236;
RX	Reading P.C., Khanna A., Smith G.L.;
RA	"Vaccinia virus encodes a soluble and cell surface tumour necrosis
RL	factor receptor that contributes to viral virulence.";
RL	Virology 292:285-298(2002).
DR	EMBL; AJ416893; CAC95181.2; -
DR	HSSP; Q29356; IJMA.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR	GO; GO:0006915; P:apoptosis; IEA.
DR	GO; GO:0006955; P:immune response; IEA.
DR	GO; GO:0007165; P:signal transduction; IEA.
DR	Pfam; PF00020; TNFR_c6; 2.
DR	PRINTS; PR01680; FASRECEPTOR.
DR	SMART; SM00208; TNFR; 2.

Qy	153	LLCSRRDTCGTCCLPGFYEHGDG-CWSC	179
Db	136	--IPKRRCPG-YFGGIDEQGNPICKSC	160
<p>RESULT 8</p> <p>072735 PRELIMINARY; PRT; 186 AA.</p>			
DT	01-AUG-1998	(T-EMBLrel. 07, Created)	
DT	01-AUG-1998	(T-EMBLrel. 07, Last sequence update)	
DT	01-MAR-2004	(T-EMBLrel. 26, Last annotation update)	
DE	A56R protein.		
GN	Name=A56R;		
OS	Cowpox virus (CPV).		
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;		
OC	Orthopoxvirus.		
OX	NCBI_TaxID=10243;		
OX	{1}		
RN	SEQUENCE FROM N.A.		
RP	STRAIN=GRI-90;		
RC	MEDLINE=98229462; PubMed=9568042; DOI=10.1006/viro.1998.9039;		
RX	Sichelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,		
RA	Ryazankina O.I., Gutorov V.V., Kotwal G.J.,		
RA	Sichelkunov S.N., Sandakhchiev L.S.,		
RA	"genes of a circle of hosts for the cowpox virus.";		
RT	smallpox, and vaccinia viruses.";		
RT	Virology 243:432-460(1998).		
RN	{3}		
RN	SEQUENCE FROM N.A.		
RP	STRAIN=GRI-90;		
RC	MEDLINE=98229462; PubMed=9568042; DOI=10.1006/viro.1998.9039;		
RX	Sichelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,		
RA	Ryazankina O.I., Gutorov V.V., Kotwal G.J.,		
RA	Sandakhchiev L.S.;		
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; X94355; CAD90723.1; --		
DR	HSP; Q92956; luma.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	InterPro; IPR001368; TNFR_c6.		
DR	Pfam; PF00020; TNFR_c6; 2.		
DR	SMART; SM00208; TNFR; 2.		
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.		
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.		
SQ	SEQUENCE 186 AA; 20482 MW; D2342F1040A00AE3 CRC64;		
<p>Query Match 13.7%; Score 155; DB 2; Length 186;</p> <p>Best Local Similarity 23.9%; Pred. No. 2.1e-05;</p> <p>Matches 39; Conservative 20; Mismatches 62; Indels 42; Gaps 7</p>			
Qy	33	CDACAGDPHKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARC	92
Db	37	CD-EGEYLDKRHNQCCNQCPEPAKVRCS-GSDNTKRCRCPHTYTAIPNYSNG-CHQC	93
Qy	93	QACDEQASVALENCNSAVATRCCKPQFWFECVQSCVSSSPFCQCLDCGALHRRTR	152
Db	94	RKCPTGSDFKV-KCTQTQNSKCSCLPGWY-----CATD-----	125
Qy	153	LLCSRRDTCGTCCLPGFYEHGDGCVSPTSTLGSFCRPERCAAVC	195
Db	126	---SSQTEDCEDCDVPK-----SRCPGCGYGGIDEQGNPIC	157
<p>RESULT 9</p> <p>Q9YP87 PRELIMINARY; PRT; 186 AA.</p>			
ID	Q9YP87		
AC	Q9YP87		

Db 94 RKCPGTFDKV--KCTQTQNSKSCSLPGWF-----CATDSS-KTEDCRDC-----133

Qy 153 LLGSRRTDCGTCCLPGFYEHGDG-CVSC 179

Db 136 --IPKRKPCPG-YFGGIDELGNPLKSC 160

RESULT 10

Q7ZZY4 PRELIMINARY; PRT; 146 AA.

ID Q7ZZY4 AC Q7ZZY4; 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Osteoprotegerin (Fragment).

OS Name=OPG;

GN Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22760275; PubMed=12878204; DOI=10.1016/S0006-291X(03)01304-4;

RA Bridgman J.T.; Johnson A.L.;

RT "Characterization of chicken TNFR superfamily decoy receptors, DcR3

RL Biochem. Biophys. Res. Commun. 307:956-961(2003).

EMBL: AV251407; AAP03890.1; -

DR HSP; O14763; ID4V.

GO: GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 2.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.

DR PROSITE; PSS0050; TNFR\_NGFR\_2; 2.

FT NON TER 146 146

SQ SEQUENCE 146 AA; 16487 MW; 1C9E64FE3A0FC2DF CRC64;

Query Match 13.0%; Score 146.5; DB 2; Length 146;

Best Local Similarity 28.3%; Pred. No. 9e-05;

Matches 39; Conservative 13; Mismatches 49; Indels 37; Gaps 7

Qy 48 CRGCPAGHYLKAPCTEPCGNSTCLVCQDTPFLAWENHNSCARCOA-CDEQASQVALEN 106

Db 41 CQCQPPGSYVKHCT-AASFVCAACP-DQYAEADWNSDQCYSVCKE--LQYIKOE 96

Qy 107 CSAVADTRCCGCKPGWFVECVQSVSCVSSPFYQCPLDCGALHRLHTRLLCSRRDTC- 162

Db 97 CTSTQDRVRCIEGWYLELEF-----CL-----KHTECPPGF 128

Qy 163 GTCLPGFYEHGDGCVSCP 180

Db 129 GVAQPGTFESDITVCFCCP 146

RESULT 11

Q9JKE0 PRELIMINARY; PRT; 169 AA.

ID Q9JKE0 AC Q9JKE0; 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE CD40 protein (Fragment).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Wistar; TISSUE=Smooth muscle;

```
RX MEDLINE=99330195; PubMed=10403401; DOI=10.1016/S0014-5793(99)00683-3;
RA Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.;
RT "Cytokine-inducible CD40 gene expression in vascular smooth muscle
cells is mediated by nuclear factor kappaB and signal transducer and
activator of transcription-1.";
RL FEBS Lett. 453:191-196(1999).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Smooth muscle;
RA Gao D., Hecker M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241231; AAFA43717.2; -.
DR HSSP; Q92956; 1JMA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR008063; F: Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
DR PROSITE; PS0652; TNFR_NGFR_1; 1.
DR PROSITE; PS0050; TNFR_NGFR_2; 3.
FT NON TER 169
SQ SEQUENCE 169 AA; 1825 MW; F199D91EFA224A26 CRC64;

Query Match 12.2%; Score 137.5; DB 2; Length 169;
Best Local Similarity 29.1%; Pred. No. 0.00058;
Matches 51; Conservative 15; Mismatches 78; Indels 31; Gaps 9;

Qy 5 PRGCAVAAMALLVLGARAAGGTRPRCDACAGFHKKIGLFCRCGCPAGHYLKAPTETP 64
Db 5 POLCALMGCLLTAVHLG-----QCVTCSDKYQLQGECDCDLCOPGNRLVSHCT-A 53

Qy 65 CGNSTCLVCPQDTFLAVENHNSE--CARQACD-EQASQVALENCASAVADTRCGCKPGW 121
Db 54 LEKTCQCPDSDGERSA---HWNRIHQHCHLQGLVKKEG-TAVSDTVCTCKEG- 108

Qy 122 FVEQVSCVSSSPFYCQPCLD----CGALHHRHLLCSRRDTCGTCLPGFYEHG 173
Db 109 -----QHCASKE---CETCAQHRPCGPGFGVQWQVATETDTCVQCPGVGFFSNG 154

RESULT 12
Q8SQ51 PRELIMINARY; PRT; 124 AA.
AC Q8SQ51;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fas deltae (Fragment).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
RT "Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
cells.";
RL Eur. J. Immunogenet. 31:159-166(2004).
DR EMBL; AB072010; BAB86799.1; -.
DR HSSP; O14763; 1DQG.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6; 2.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
FT NON TER 1
SQ SEQUENCE 147 AA; 16751 MW; 0E192AC4DCE1001F CRC64;

Query Match 11.8%; Score 133.5; DB 2; Length 147;
Best Local Similarity 29.4%; Pred. No. 0.0011;
Matches 30; Conservative 12; Mismatches 23; Indels 37; Gaps 5;

Qy 83 NHNSCARQACDEQASQVALENCASAVADTRCGCKPGWFVECVSCVSSSPFYCQPC 142
Db 10 SHFSPRCRCKICDEEHGLEVKENCTRTQNTKCKSKNFP--CNVSQC-----DHCNPCM 62

Qy 143 DCGALHHRHLLCSRRDTCGTCLPGFYEHG--DGCVCSCPTS 182
Db 63 MC-----EHGILENCT--PTS 76

RESULT 13
Q8SQ52 PRELIMINARY; PRT; 147 AA.
AC Q8SQ52;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fas (Fragment).
OC Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
RT "Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
cells.";
RL Eur. J. Immunogenet. 31:159-166(2004).
DR EMBL; AB072009; BAB86798.1; -.
DR HSSP; O14763; 1D4V.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
FT NON TER 1
SQ SEQUENCE 147 AA; 16751 MW; 0E192AC4DCE1001F CRC64;

Query Match 11.8%; Score 133.5; DB 2; Length 147;
Best Local Similarity 29.4%; Pred. No. 0.0011;
Matches 30; Conservative 12; Mismatches 23; Indels 37; Gaps 5;

Qy 83 NHNSCARQACDEQASQVALENCASAVADTRCGCKPGWFVECVSCVSSSPFYCQPC 142
Db 10 SHFSPRCRCKICDEEHGLEVKENCTRTQNTKCKSKNFP--CNVSQC-----DHCNPCM 62

Qy 143 DCGALHHRHLLCSRRDTCGTCLPGFYEHG--DGCVCSCPTS 182
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DR EMBL; AF084992; AAP09112.1; -.
DR HSSP; Q92956; 1JMA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 176 AA; 19535 MW; 83C2168F11D0B072 CRC64;

Query Match 11.3%; Score 128; DB 2; Length 176;
Best Local Similarity 33.3%; Pred. No. 0.0037;
Matches 31; Conservative 15; Mismatches 35; Indels 12; Gaps 6;

QY 26 GGRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAPCTPCGNSGTCILVCPDPTFLAWENHH 85
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 18 GGSKM----CKPD-EVYLGNCQCPGSGGQKTKVCTENSG-ITCTLCPNGTYLT--GLY 69
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

QY 86 NSECARCQACDEQASQVALENCASAVADTRCGCK 118
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 70 N--CTNCTQCD--TQITVRNCTSTNTTICASK 98
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

Search completed: June 27, 2005, 13:59:20
Job time : 172 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2005, 13:44:28 ; Search time 162 Seconds  
(without alignments)

465.545 Million cell updates/sec

Title: US-10-081-280-6\_COPY\_1\_195

Perfect score: 1130

Sequence: 1 MEQPRGCAVAALLLVLL.....CVSCTSTLSCPCRAA VC 195

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1426428

Minimum DB seq length: 0

Maximum DB seq length: 195

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1051	93.0	181	2	AAW26708 Human apo
2	1051	93.0	181	6	ABG73992 Human APO
3	1051	93.0	181	6	ABU08251 Human APO
4	1051	93.0	181	6	ABG73857 Human APO
5	1051	93.0	181	6	ABU10202 Human APO
6	1051	93.0	181	6	ADA49687 Human APO
7	1051	93.0	188	5	AAO17880 Human rhe
8	206.5	18.3	161	6	ABR62365 Tumour ne
9	200.5	17.7	154	3	AAAY94711 Tumour ne
10	200.5	17.7	154	6	ADA49698 Extracell
11	200.5	17.7	154	7	ADL17741 Human tum
12	200.5	17.7	154	8	ADJ56814 Human TNF
13	200.5	17.7	161	2	ABG74752 Human TNF
14	200.5	17.7	161	2	AAR27496 Native 30
15	200.5	17.7	161	2	AAW59664 Human sol
16	200.5	17.7	161	2	AAW52267 Soluble t
17	200.5	17.7	161	2	AAW89233 Tumour ne
18	200.5	17.7	161	4	AB37676 Human 30
19	200.5	17.7	161	6	ABR62363 Tumour ne
20	200.5	17.7	161	6	ADA20577 Human 30k
21	200.5	17.7	161	6	ADA20579 Human 30k
22	200.5	17.7	161	8	ADH78698 Human tum
23	198.5	17.6	162	5	AAW48058 Human TNF
24	197.5	17.5	161	6	ABR62364 Tumour ne
25	197	17.4	32	4	AAW84943 Human TR3

ALIGNMENTS

RESULT 1  
AAW26708  
ID AAW26708 standard; protein; 181 AA.  
XX  
AC AAW26708;  
XX  
DT 14-APR-1998 (first entry)  
XX  
DE Human apoptosis protein Apo-2LI.  
XX  
KW Apo-2LI; apoptosis; Apo-2 ligand inhibitor; human; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= Sig\_peptide  
FT Modified-site 67  
FT /note= "N-glycosylated"  
FT Modified-site 106  
FT /note= "N-glycosylated"  
XX  
PN WO9737020-A1.  
XX  
PD 09-OCT-1997.  
XX  
PF 31-MAR-1997; 97WO-US005230.  
XX  
PR 01-APR-1996; 96US-00625328.  
PR 23-SEP-1996; 96US-00710802.  
XX  
(GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ;  
XX  
DR WPI; 1997-503105/46.  
XX  
DR N-ESDB; AAT91179.  
XX  
PT Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis in mammalian cells.  
XX  
PS Claim 1; Page 43-44; 70pp; English.  
XX  
CC This novel polypeptide, designated Apo-2 ligand inhibitor (Apo-2LI), can be used to inhibit apoptosis for therapeutic purposes. Its amino acid sequence was deduced from a human thymus cDNA clone (see AAT91179) and is identical to amino acid residues 1-181 of another novel apoptosis polypeptide, Apo-3 (see AAW26709). It may be a soluble, truncated of

26	196	17.3	139	4	AAB66977	Aab66977 Peptide:
27	196	17.3	139	5	ABG71825	Abg71825 Wild type
28	196	17.3	139	8	ADM28814	Adm28814 Human TNF
29	191	16.9	181	5	ABB98170	Abb98170 Soluble b
30	191	16.9	181	5	AAE25817	Aae25817 Bovine tu
31	190	16.8	32	8	ADH50950	Adh50950 Altered T
32	186	16.5	185	7	ADJ65993	Adj65993 Herpes vi
33	186	16.5	186	3	AAAY79206	Aay79206 Soluble h
34	186	16.5	186	6	ABU60688	Abu60688 Human sol
35	186	16.5	186	7	ADF50687	Adf50687 Soluble f
36	186	16.5	193	3	AAAY79204	Aay79204 Soluble h
37	186	16.5	193	6	ABU60675	Abu60675 Human sol
38	186	16.5	193	7	ADF50685	Adf50685 Soluble f
39	182	16.1	148	6	ABU60689	Abu60689 Human mat
40	182	16.1	155	6	ABU60676	Abu60676 Human mat
41	182	16.1	159	6	ABU60683	Abu60683 Human mat
42	175.5	15.5	159	2	AAAR24083	Aar24083 Truncated
43	175	15.5	170	3	ABAB36228	Abab36228 Rat Fas r
44	174.5	15.4	161	7	ADL17744	Adl17744 Human TRA
45	174.5	15.4	161	8	ADJ56817	Adj56817 Human TR2

CC secreted form of Apo-3, lacking some extracellular sequence as well as  
CC the transmembrane and cytoplasmic sequences of Apo-3. Apo-2LI can be  
CC produced in host cells using a claimed method. Chimeric polypeptides  
CC comprising Apo-2LI fused to a heterologous amino acid sequence, and an  
CC Apo-2LI dimer are also claimed. Apo-2LI can be used to inhibit mammalian  
CC cell apoptosis in vivo or ex vivo, and in quantitative diagnostic assays  
XX  
SQ Sequence 181 AA;

Query Match 93.0%; Score 1051; DB 2; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.8e-72;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
DB 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASAVADTRCGCKPG 120  
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASAVADTRCGCKPG 120  
QY 121 WFVECVSQVSSSPFFYCQPCDCLGALHRRHRLILCSRRDTCGTLPGFYEHGDCVSCP 180  
DB 121 WFVECVSQVSSSPFFYCQPCDCLGALHRRHRLILCSRRDTCGTLPGFYEHGDCVSCP 180  
QY 181 T 181  
DB 181 T 181

RESULT 2  
ABG73992  
ID ABG73992 standard; protein; 181 AA.

AC ABG73992;  
XX  
XX 01-APR-2003 (first entry)  
XX Human APO-2 ligand inhibitor (Apo2LI) protein.  
XX APO-2LI; human; apoptosis; monoclonal antibody; Apo-2 ligand inhibitor;  
KW cytostatic; cancer; autoimmune; inflammatory; neurodegenerative disease.  
KW  
XX Homo sapiens.  
XX  
XX US6469144-B1.  
XX  
XX 22-OCT-2002.  
XX  
XX 31-MAR-1997; 97US-00828683.  
XX  
XX 01-APR-1996; 96US-00625328.  
XX 23-SEP-1996; 96US-00710802.  
XX

XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ;  
XX  
XX WPI; 2003-147110/14.  
XX N-PSDB; ABX15839.  
XX  
XX Novel isolated monoclonal antibody useful for activating or stimulating  
XX apoptosis in cancer cells, comprises an antigen binding site which binds  
XX to an Apo-2 ligand inhibitor polypeptide or to an Apo-3 polypeptide.  
XX  
XX Claim 1; Fig 1; 48pp; English.

XX This invention relates to an isolated monoclonal antibody comprising an  
XX antigen binding site which binds to an Apo-2 ligand inhibitor (Apo-2LI)  
XX polypeptide. The antibody of the invention may have cytostatic activity  
XX and may act as an activator or stimulator of apoptosis in cancer cells,  
XX as a blocker of excessive apoptosis or of the autoimmune/inflammatory  
XX effects of Apo-3 resulting from nuclear factor (NF)-kappaB activation or

CC C-Jun-amino-terminal kinase (JNK) activation. The anti-Apo-2 ligand  
CC inhibitor is useful in therapeutic purposes for activating or stimulating  
CC apoptosis in cancer cells and may be used to block excessive apoptosis  
CC (for example in neurodegenerative disease), or to block potential  
CC autoimmune/inflammatory effects of Apo-3 resulting from nuclear factor  
CC (NF)-kappaB activation or C-Jun-amino-terminal kinase (JNK) activation.  
CC The antibody may also be used in diagnostic assays for Apo-2LI or Apo-3,  
CC e.g. detecting Apo-2LI or Apo-3 expression in specific cells, tissues or  
CC serum, or for affinity purification of Apo-2LI or Apo-3 from recombinant  
CC cell culture or natural sources. The present sequence represents the  
CC human Apo-2 ligand inhibitor protein (Apo2-LI) which was used to generate  
CC the antibody of the invention  
XX

SQ Sequence 181 AA;

Query Match 93.0%; Score 1051; DB 6; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.8e-72;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
DB 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASAVADTRCGCKPG 120  
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASAVADTRCGCKPG 120  
QY 121 WFVECVSQVSSSPFFYCQPCDCLGALHRRHRLILCSRRDTCGTLPGFYEHGDCVSCP 180  
DB 121 WFVECVSQVSSSPFFYCQPCDCLGALHRRHRLILCSRRDTCGTLPGFYEHGDCVSCP 180  
QY 181 T 181  
DB 181 T 181

RESULT 3  
ABU08251  
ID ABU08251 standard; protein; 181 AA.

AC ABU08251;  
XX  
XX 13-MAY-2003 (first entry)  
XX Human Apo-2 ligand inhibitor, Apo-2LI.

XX Human; Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; AIDS;  
KW acquired immunodeficiency syndrome; stroke; Alzheimer's disease; cancer;  
KW Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis;  
KW retinitis pigmentosa; aplastic anaemia; cerebellar degeneration;  
KW myocardial infarction; reperfusion injury; toxin-induced liver disease;  
KW chromosome 1q36.3; programmed cell death.  
XX

XX Homo sapiens.  
XX  
XX US2002165157-A1.  
XX  
XX 07-NOV-2002.  
XX  
XX 21-FEB-2002; 2002US-00081280.  
XX  
XX 01-APR-1996; 96US-0014699P.  
XX 23-SEP-1996; 96US-0026943P.  
XX 31-MAR-1997; 97US-00829270.  
XX

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ;  
XX  
XX WPI; 2003-298703/29.  
XX N-PSDB; ABX13176.  
XX New biologically active Apo-2LI or Apo-3 polypeptide, useful for

PT preparing a composition for treating cancer.

XX Claim 4; Fig 1; 45pp; English.

XX The invention relates to an new isolated biologically active Apo-2LI or  
XX Apo-3 having at least 80 % sequence identity with native sequence Apo-2LI or  
XX Apo-3 appearing as AB008251 and AB008252. Also included are a  
XX chimeric molecule comprising the Apo-2LI fused to a heterologous amino  
XX acid sequence; a dimer molecule comprising a first Apo-2LI and a second  
XX Apo-2LI; an antibody that binds to Apo-2LI or Apo-3 (or to its  
XX extracellular domain sequence), an isolated nucleic acid encoding Apo-2LI  
XX or Apo-3, a vector comprising the nucleic acid, a host cell comprising  
XX the vector, a method of producing Apo-2LI and a non-human (transgenic or  
XX knockout) animal that contains cells that express nucleic acid encoding  
XX Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3  
XX are involved in apoptosis (programmed cell death) which is implicated in  
XX AIDS, (acquired immunodeficiency syndrome), stroke, Alzheimer's disease,  
XX Parkinson's disease, amyotrophic lateral sclerosis, multiple sclerosis,  
XX retinitis pigmentosa, aplastic anaemia, cerebellar degeneration,  
XX myocardial infarction, reperfusion injury and toxin-induced liver  
XX disease. The gene for both proteins is located on chromosome 1q36.3 Apo-  
XX 2LI and Apo-3 are also useful for preparing a composition for treating  
XX cancer. The present sequence represents Apo-2LI

XX Sequence 181 AA;

Query Match 93.0%; Score 1051; DB 6; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.8e-72;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60  
DB 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60  
QY 61 CTEPCGNSTCLVCPDPTFLAENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120  
DB 61 CTEPCGNSTCLVCPDPTFLAENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120  
QY 121 WFVEQVQSVCSSSPFFYQPCDCLDGCALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180  
DB 121 WFVEQVQSVCSSSPFFYQPCDCLDGCALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180  
QY 181 T 181  
DB 181 T 181

RESULT 4

ABG73857

ID ABG73857 standard; protein; 181 AA.

XX AC ABG73857;

XX DT 03-APR-2003 (first entry)

XX DE Human Apo-2 ligand inhibitor protein.

XX KW Human; Apo-2; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;  
XX tumour necrosis factor receptor; nuclear factor-kappa B; NF-kappa B;  
XX Apo-2 ligand inhibitor; AIDS; acquired immunodeficiency syndrome;  
XX Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
XX multiple sclerosis; retinitis pigmentosa; cerebellar degeneration;  
XX aplastic anaemia; myocardial infarction; stroke; reperfusion injury;  
XX toxin-induced liver disease; cancer; lupus; herpes virus infection.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 67

FT Modified-site /note= "N-glycosylated"

FT Modified-site 105

FT /note= "N-glycosylated. The amino acid at residue 105 is  
FT Glu not Asn"

XX US6462176-B1.

XX PD 08-OCT-2002.

XX PF 11-SEP-1997; 97US-00928069.

XX PR 23-SEP-1996; 96US-0026943P.

XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi AJ;

XX DR WPI; 2003-173840/17.

XX N-PSDB; ABX15460.

XX Novel isolated Apo-3 polypeptide useful for inducing apoptosis in  
XX mammalian cells, for generating antibodies, in affinity purification  
XX techniques, and in competitive-type receptor binding assays.

XX Example 1; Fig 1; 52pp; English.

XX The invention relates to an Apo-3 polypeptide having an extracellular  
XX domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide  
XX has been found to stimulate or induce apoptotic activity in mammalian  
XX cells. Human Apo-3 exhibits similarities to the tumour necrosis factor  
XX receptor (TNFR) family of polypeptides. The invention also relates to a  
XX chimeric molecule comprising an extracellular domain sequence comprising  
XX residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The  
XX Apo-3 polypeptide is useful therapeutically to induce apoptosis in  
XX mammalian cells. Decreased levels of apoptosis has been associated with  
XX conditions such as cancer, lupus, and herpes virus infection. Increased  
XX levels of apoptosis are associated with diseases such as acquired  
XX immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's  
XX disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis  
XX pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial  
XX infarction, stroke, reperfusion injury, and toxin-induced liver disease.  
XX The Apo-3 polypeptide is also useful in non-therapeutic applications such  
XX as in quantitative diagnostic assays as a control against which samples  
XX containing unknown quantities of Apo-3 may be prepared, in generating  
XX antibodies, as standards in assays for Apo-3, in affinity purification  
XX techniques, and in competitive-type receptor binding assays. The chimeric  
XX molecule is useful therapeutically to inhibit apoptosis or nuclear factor  
XX -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-  
XX Apo-3 antibodies. The present sequence represents the human Apo-2 ligand  
XX inhibitor protein which comprises amino acid residues 1 to 181 of the  
XX human Apo-3 protein. It is believed that Apo-2 ligand inhibitor may be a  
XX soluble, truncated or secreted form of Apo-3

XX Sequence 181 AA;

Query Match 93.0%; Score 1051; DB 6; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.8e-72;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60

DB 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPDPTFLAENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120

DB 61 CTEPCGNSTCLVCPDPTFLAENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120

QY 121 WFVEQVQSVCSSSPFFYQPCDCLDGCALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180

DB 121 WFVEQVQSVCSSSPFFYQPCDCLDGCALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180

QY 181 T 181

DB 181 T 181

RESULT 5

ABU10202  
ID ABU10202 standard; protein; 181 AA.  
XX  
AC ABU10202;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
XX  
DE Human Apo-2 ligand inhibitor.  
XX  
XX  
KW Human; Apo-2 ligand inhibitor; apoptosis; gene therapy; inflammation;  
KW cancer; neurodegenerative disease; immunosuppressive; tissue typing.  
XX  
OS Homo sapiens.  
XX  
XX  
PN US2003004313-A1.  
XX  
XX  
PD 02-JAN-2003.  
XX  
XX  
XX 28-MAR-2002; 2002US-00112193.  
XX  
XX 23-SEP-1996; 96US-0026943P.  
XX 11-SEP-1997; 97US-00928069.  
XX  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX  
PI Ashkenazi AJ;  
XX  
XX WPI; 2003-438872/41.  
DR N-PSDB; ACA61684.  
XX  
XX  
PT New isolated Apo-3 polypeptides, useful for stimulating or inducing  
PT apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo  
PT or ex vivo gene therapy techniques.  
XX  
XX  
PS Example 1; Fig 1; 50pp; English.  
XX  
XX  
CC The invention relates to an isolated Apo-3 polypeptide. The Apo-3  
CC polypeptides are useful for stimulating or inducing apoptotic activity in  
CC mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy  
CC techniques. The Apo-3 chimeric molecules are useful for inhibiting  
CC apoptosis, or as immunogens used in generating antibodies. The  
CC antagonistic antibodies may be used to block excessive apoptosis, for  
CC instance in neurodegenerative disease, or to block potential autoimmune/  
CC inflammatory effects of Apo-3 resulting from NF-kappaB activation. The  
CC nucleic acid sequences are useful as diagnostics for tissue-specific  
CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or  
CC knockout animals.. The transgenic or knockout animals are useful in  
CC developing and screening of therapeutically useful reagents. The present  
CC sequence represents the amino acid sequence of human Apo-2 ligand  
CC inhibitor  
XX  
SQ Sequence 181 AA;  
  
Query Match 93.0%; Score 1051; DB 6; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.8e-72;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MEQPRGCAAAVAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
DB 1 MEQPRGCAAAVAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
  
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120  
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120  
  
QY 121 WFVECVQSQVSSSPFYCQPCLDGALHRRLLCSRRDTCGTCPLGFEYHGGCVSCP 180  
DB 121 WFVECVQSQVSSSPFYCQPCLDGALHRRLLCSRRDTCGTCPLGFEYHGGCVSCP 180  
  
QY 181 T 181  
DB 181 T 181

RESULT 6  
ADA49687  
ID ADA49687 standard; protein; 181 AA.  
XX  
AC ADA49687;  
XX  
XX  
DT 20-NOV-2003 (first entry)  
XX  
XX  
DE Human Apo-2 ligand inhibitor (Apo-2LI) .  
XX  
XX  
KW Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity;  
KW competitive-type receptor; binding assay; cancer cell; human; cytostatic.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
XX US2002192729-A1.  
XX  
XX 19-DEC-2002.  
XX  
XX 28-MAR-2002; 2002US-00112793.  
XX  
XX 01-APR-1996; 96US-00625328.  
XX 23-SEP-1996; 96US-00710802.  
XX 31-MAR-1997; 97US-00828683.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ;  
XX  
XX WPI; 2003-657226/62.  
DR N-PSDB; ADA49691.  
XX  
XX  
PT Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or  
PT Apo-3 polypeptide which induces or stimulates apoptotic activity, useful  
PT in diagnostic assays.  
XX  
XX  
PS Claim 4; Fig 1; 53pp; English.  
XX  
XX  
CC The present invention relates to the isolation of a biologically active  
CC Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide  
CC sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The  
CC Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI  
CC is useful for generating antibodies, as standards in assays for Apo-3 or  
CC Apo-2LI, in affinity purification techniques, and in competitive-type  
CC receptor binding assays when labelled with radioiodine, enzymes or  
CC fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or  
CC inducing apoptosis in cancer cells, and thus have therapeutic utility.  
CC The present sequence represents human Apo-2LI.  
XX  
SQ Sequence 181 AA;  
  
Query Match 93.0%; Score 1051; DB 6; Length 181;  
Best Local Similarity 100.0%; Pred. No. 4.8e-72;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MEQPRGCAAAVAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
DB 1 MEQPRGCAAAVAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
  
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120  
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120  
  
QY 121 WFVECVQSQVSSSPFYCQPCLDGALHRRLLCSRRDTCGTCPLGFEYHGGCVSCP 180  
DB 121 WFVECVQSQVSSSPFYCQPCLDGALHRRLLCSRRDTCGTCPLGFEYHGGCVSCP 180  
  
QY 181 T 181  
DB 181 T 181

RESULT 7  
ID AAO17880  
AAO17880 standard; protein; 188 AA.  
AC AAO17880;  
XX  
DT 22-AUG-2002 (first entry)  
XX  
DE Human rheumatoid arthritis associated DR3 gene related protein #2.  
XX  
KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200234912-A1.  
XX  
PD 02-MAY-2002.  
XX  
PF 24-OCT-2001; 2001WO-JP009313.  
XX  
PR 24-OCT-2000; 2000JP-00324296.  
XX  
PR 27-MAR-2001; 2001JP-00090546.  
XX  
PR 30-MAR-2001; 2001JP-00099990.  
XX  
PA (NEWI-) NEW IND RES ORG.  
PA (SHIO/) SHIOZAWA S.  
XX  
PI Shiozawa S, Konishi Y;  
XX  
XX WPI; 2002-417132/44.  
DR N-PSDB; AAL47187.  
XX  
XX Genomes, particularly DR3 genomic DNA, participating in rheumatoid  
PT arthritis via mutation, useful in evaluating disease onset and its  
PT possibility and providing therapy and remedies.  
XX  
PS Disclosure; Page 72-73; 84pp; Japanese.  
CC  
CC The present invention relates to the human DR3 gene, which is associated  
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to  
CC the disease. The sequences can be used to evaluate disease onset and its  
CC possibility and to provide therapy and remedies. The present sequence is  
CC a protein described in the exemplification of the invention  
XX  
XX Sequence 188 AA;  
Query Match 93.0%; Score 1051; DB 5; Length 188;  
Best Local Similarity 100.0%; Pred. No. 5e-72;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEQPRGCAVAAALLVLLGARAAGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60  
DB 1 MEQPRGCAVAAALLVLLGARAAGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60  
QY 61 CTEPCGNTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCSAVADTRCGCKPG 120  
DB 61 CTEPCGNTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCSAVADTRCGCKPG 120  
QY 121 WFVEQVQCVSSSPFYCQPCLDGALHRLTLLCSRRDTCGTCLPGFYEHGDCVSCP 180  
DB 121 WFVEQVQCVSSSPFYCQPCLDGALHRLTLLCSRRDTCGTCLPGFYEHGDCVSCP 180  
QY 181 T 181  
DB 181 T 181  
RESULT 8  
ABR62365  
ID ABR62365 standard; protein; 161 AA.  
XX  
AC ABR62365;

XX  
DT 22-SEP-2003 (first entry)  
XX  
DE Tumour necrosis factor receptor extracellular domain H23P mutant.  
XX  
KW Tumour necrosis factor; receptor; TNFR<sub>ED</sub>; proline; protein engineering;  
KW mutant; mutein.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 23 /note= "wild-type His substituted by Pro"  
FT Misc-difference 46 /note= "wild-type Ser substituted by Ile"  
FT  
XX  
PN WO2003046160-A2.  
XX  
XX 05-JUN-2003.  
XX  
PF 21-NOV-2002; 2002WO-EP013059.  
XX  
PR 30-NOV-2001; 2001US-0340648P.  
XX  
XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.  
XX  
PI Brondyk W, Jiang X, Schweickhardt RL;  
XX  
XX WPI; 2003-523245/49.  
XX  
XX Increasing expression of a protein, comprises substituting at least one  
PT codon in the polynucleotide encoding the protein, for a codon encoding  
PT proline.  
XX  
PS Example 2; Page; 53pp; English.  
XX  
CC This is the protein sequence of a mutated extracellular domain of the p55  
CC tumour necrosis factor receptor (TNFR<sub>ED</sub>) in which a Pro residue  
CC substitutes the native His-34 residue (residue 23 in the present  
CC sequence) and an Ile residue substitutes the native Ser-57 residue  
CC (residue 46 of the present sequence). Screening of TNFR<sub>ED</sub> mutant clones  
CC using a yeast display system yielded a clone that showed a higher  
CC expression level in yeast than did a wild-type TNFR<sub>ED</sub> clone. The encoded  
CC polypeptide contained these 2 amino acid substitutions. The introduction  
CC of proline residues may assist the polypeptide to adopt a favourable  
CC conformation that fixes the neighbouring cysteine residue into the  
CC correct orientation for disulfide bond formation, resulting in a higher  
CC yield of correctly folded proteins in yeast or mammalian host cells. The  
CC invention therefore provides methods of increasing protein expression  
CC levels by substituting an amino acid residue with proline, where the  
CC substitution occurs within 15 (preferably within 10, and especially  
CC within 5) amino acids of a cysteine residue. Note: The present sequence  
CC is not shown in the specification but is derived from the TNFR<sub>ED</sub> sequence  
CC given in figure 4 (see ABR62363)  
XX  
XX Sequence 161 AA;  
Query Match 18.3%; Score 206.5; DB 6; Length 161;  
Best Local Similarity 30.4%; Pred. No. 4.4e-08;  
Matches 49; Conservative 20; Mismatches 71; Indels 21; Gaps 7;  
QY 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNTCLVCPQDTFLAWENHNSECARQACDQQA 99  
DB 11 HPQNNSTCCTKCPKGTLYNDPCPGQDTCREIGSGFTASENHLR-HCLSCSKCKREM 69  
QY 100 SQVALENCASVADTRCGCKPGWFVEEC---QVSQCVSSSPFYCQPCLDGALHRLTLLCS 156  
DB 70 GQVEISSCTVDRDTCVCGCRKQRYHNSENLFCQ-----FNCSLCLN-GTVH----LSCQ 119  
QY 157 RRDTCGTCCLPGFYEHGDCVSCPSTLGSQCP---RCAAVC 195  
DB 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 155

RESULT 9  
AAY94711  
ID AAY94711 standard; protein; 154 AA.  
XX AC AAY94711;  
XX DT 29-JAN-2001 (first entry)  
XX DE Tumour necrosis factor receptor (TNFR) domain of TNFR-1.  
XX KW Tumour necrosis factor-receptor related protein; TR2; human; cancer;  
XX KW chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;  
XX KW immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;  
XX KW severely combined immunodeficiency; apoptosis inhibition;  
XX KW Alzheimer's disease; Parkinson's disease; Crohn's disease.  
XX OS Homo sapiens.  
XX WO200056405-A2.  
XX PD 28-SEP-2000.  
XX PF 22-MAR-2000; 2000WO-US007521.  
XX PR 22-MAR-1999; 99US-0125683P.  
XX PR 26-MAR-1999; 99US-0126522P.  
XX PR 20-MAY-1999; 99US-0135169P.  
XX PR 06-AUG-1999; 99US-0147383P.  
XX PA (NIJ/J) NI J.  
XX PA (ROSE/) ROSEN C A.  
XX PA (GENT/) GENTZ R L.  
XX PI Ni J, Rosen CA, Gentz RL;  
XX WPI; 2000-594519/56.  
XX Nucleic acid molecule encoding a human tumor necrosis factor receptor 2  
XX and its two splice variants, useful for treating arthritis or  
XX inflammation, cancer (such as follicular lymphomas) and immunodeficiency  
XX disorders.  
XX Disclosure; Fig 16; 373pp; English.  
XX This invention relates to an isolated nucleic acid molecule encoding a  
XX human tumour necrosis factor (TNF)-receptor related protein TR2. Included  
XX in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.  
XX The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a  
XX member of the TNFR superfamily. The invention includes a method for the  
XX treatment of arthritis or inflammation using an antibody directed against  
XX a fragment of the TR2 protein. TR2 its agonists, antagonists and  
XX antibodies exhibit cytostatic, dermatological, antianaemic,  
XX immunosuppressive, anti-allergic, antiarthritic, antiasthmatic,  
XX antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and  
XX cerebroprotective activity. The methods are useful for treating arthritis  
XX or inflammation, cancer (such as follicular lymphomas, carcinoma with p53  
XX mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an  
XX immunodeficiency or for enhancing an in vivo leukocyte response to an  
XX antigen. Anti-TR2 antibodies are useful for treating, inhibiting or  
XX preventing autoimmune diseases (such as autoimmune haemolytic anaemia,  
XX dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and  
XX inflammatory myopathies) and immunodeficiency disorders (such as severely  
XX combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative  
XX disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,  
XX TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or  
XX antagonists are useful for treating or preventing autoimmune diseases and  
XX inhibit the growth, progression and/or metastasis of cancers. They are  
XX also used to activate, differentiate or proliferate cancerous cells or  
XX tissues, and can be used to treat diseases associated with increased cell  
XX survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,  
XX Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful

as sources for generating antibodies, as molecular weight markers. This  
sequence represents the tumour necrosis factor receptor (TNFR) domain of  
the human TNFR-1 protein. The sequence was used in the characterisation  
of the TR2 receptor protein of the invention

Query Match 17.7%; Score 200.5; DB 3; Length 154;  
Best Local Similarity 29.8%; Pred. No. 1.2e-07;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
QY 40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQA 99  
Db 9 HPQNNISICTKCHKGTLYNDGCPGQDTCRECESGSFTASENHLR-HCLSCSKCKREM 67  
QY 100 SQVALENCNSAVATRCGCKGFWFEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCLS 156  
Db 68 GQVEISSCTVDRDTCGCRKNQRYHWSENLFC-----FNCSLCLN-GTVH-----LSCQ 117  
QY 157 RRDTDCGTCLPGFVEHGDGCVSCPTSTLGSCE--RCAAVC 195  
Db 118 EKQNTVCTCHAGFLRENECVSC-----SNCKSLECTKLC 153

RESULT 10  
ADA49698  
ID ADA49698 standard; protein; 154 AA.  
XX AC ADA49698;  
XX DT 20-NOV-2003 (first entry)  
XX DE Extracellular region of human TNFR1 (htnfr1) protein.  
XX KW Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity;  
XX KW competitive-type receptor; binding assay; cancer cell; human;  
XX KW TNF receptor family; htnfr1; cytostatic.  
XX OS Homo sapiens.  
XX FN US2002192729-A1.  
XX PD 19-DEC-2002.  
XX PF 28-MAR-2002; 2002US-00112793.  
XX PR 01-APR-1996; 96US-00625328.  
XX PR 23-SEP-1996; 96US-00710802.  
XX PR 31-MAR-1997; 97US-00828683.  
XX PA (GETH ) GENENTECH INC.  
XX FI Ashkenazi AJ;  
XX WPI; 2003-657226/62.  
XX Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or  
XX Apo-3 polypeptide which induces or stimulates apoptotic activity, useful  
XX in diagnostic assays.  
XX Disclosure; Fig 2; 53pp; English.  
XX The present invention relates to the isolation of a biologically active  
XX Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide  
XX sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The  
XX Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI  
XX is useful for generating antibodies, as standards in assays for Apo-3 or  
XX Apo-2LI, in affinity purification techniques, and in competitive-type  
XX receptor binding assays when labelled with radiolodine, enzymes or  
XX fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or  
XX inducing apoptosis in cancer cells, and thus have therapeutic utility.  
XX The present sequence represents the extracellular region of a human TNF  
XX receptor family protein. This sequence is compared with the extracellular



```
CC region of human Apo-2L1.
XX Sequence 154 AA;
SQ
    Query Match      17.7%; Score 200.5; DB 6; Length 154;
    Best Local Similarity 29.8%; Pred. No. 1.2e-07;
    Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNSECARCOACDQQA 99
DQ 9 HPQNNISICTCKHGTLYNDPCPGQDTCRECESSGFTASENHLR-HCLSCSKCKREM 67
QY 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDGCALHRRHRLCLS 156
DQ 68 GQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQC-----FNCSLCLN-GTVH----LSCQ 117
QY 157 RRDTCGTCPLGFGYEHGDCVSCPTSTLGSCEP--RCAAVC 195
DQ 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 153

RESULT 11
ID ADL17741 standard; protein; 154 AA.
XX
AC ADL17741;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human tumour necrosis factor receptor-I cysteine rich motif.
XX
KW Human; apoptosis inducing molecule II; AIM II; antibody;
KW tumour necrosis ligand superfamily; lymphotoxin-beta receptor; TR6;
KW TRAIL receptor 6; lymphadenopathy; aberrant bone development;
KW autoimmune disease; graft-versus-host disease; rheumatoid arthritis;
KW osteoarthritis; cancer; apoptosis.
XX
OS Homo sapiens.
XX
PN US635743-B1.
XX
PD 21-OCT-2003.
XX
PP 10-MAR-2000; 2000US-00523323.
XX
PR 22-MAR-1996; 96US-0013923P.
PR 31-OCT-1996; 96US-0030157P.
PR 21-MAR-1997; 97US-00822953.
PR 07-JAN-1998; 98US-00003886.
PR 20-FEB-1998; 98US-00027287.
PR 19-FEB-1998; 98US-0075409P.
PR 11-MAR-1999; 99US-00252656.
PR 04-JUN-1999; 99US-0124041P.
PR 06-JUL-1999; 99US-0137457P.
PR 11-AUG-1999; 99US-0148326P.
PR 02-DEC-1999; 99US-0168380P.
XX
(PUMA-) HUMAN GENOME SCI INC.
XX
PI Ebner R, Yu G, Ruben SM, Ullrich S, Zhai Y;
XX
WPI; 2003-810570/76.
XX
PT New antibody that binds to human Apoptosis Inducing Molecule II (AIM II)
PT protein, useful for preparing a composition for treating e.g.,
PT lymphadenopathy, autoimmune disease, rheumatoid arthritis, osteoarthritis
PT or cancer.
XX
PS Example 13; SEQ ID NO 53; 163pp; English.
XX
CC The invention relates to an isolated antibody or its portion binding to a
CC protein comprising a protein whose sequence comprises an immunogenic
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```
CC fragment of the amino acid residues 68-240 of the Human apoptosis
CC inducing molecule II, AIM II, appearing as ADL17690 or a protein whose
CC sequence comprises a fragment of amino acid residues 68-240, where the
CC fragment comprises at least 30 or 50 amino acid residues. Also included
CC are a hybridoma that produces the antibody, a method of detecting in a
CC biological sample a protein that binds the antibody or its portion, a
CC composition comprising the antibody and a carrier and an isolated cell
CC that produces the antibody. Human AIM II is a member of the tumour
CC necrosis ligand superfamily and has been shown to bind lymphotoxin-beta
CC receptor and TR6 (TRAIL receptor 6). The antibody is useful for preparing
CC a composition for treating e.g., lymphadenopathy, aberrant bone
CC development, autoimmune disease, graft-versus-host disease, rheumatoid
CC arthritis, osteoarthritis or cancer (many other diseases and conditions
CC are listed in the specification). The present sequence represents a
CC cysteine-rich motif from a protein thought to bind AIM II.
XX
SQ Sequence 154 AA;
    Query Match      17.7%; Score 200.5; DB 7; Length 154;
    Best Local Similarity 29.8%; Pred. No. 1.2e-07;
    Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNSECARCOACDQQA 99
DQ 9 HPQNNISICTCKHGTLYNDPCPGQDTCRECESSGFTASENHLR-HCLSCSKCKREM 67
QY 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDGCALHRRHRLCLS 156
DQ 68 GQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQC-----FNCSLCLN-GTVH----LSCQ 117
QY 157 RRDTCGTCPLGFGYEHGDCVSCPTSTLGSCEP--RCAAVC 195
DQ 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 153

RESULT 12
ADJ56814
ID ADJ56814 standard; protein; 154 AA.
XX
AC ADJ56814;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human TNFR-I cysteine-rich motif.
XX
KW Apoptosis inducing molecule II; AIM II; TNF; tumour necrosis factor;
KW therapy; graft versus host disease; immunodeficiency; cancer;
KW autoimmune disease; multiple sclerosis; type I diabetes;
KW rheumatoid arthritis; primary biliary cirrhosis; aplastic anaemia;
KW myelodysplasia; systemic lupus erythematosus;
KW idiopathic thrombocytopenic purpura; cellular response;
KW T-cell activation; molecular weight marker; human; TNF receptor; TNFR.
XX
OS Homo sapiens.
XX
PN US2004009147-A1.
XX
PD 15-JAN-2004.
XX
PP 28-FEB-2003; 2003US-00375680.
XX
PR 22-MAR-1996; 96US-0013923P.
PR 31-OCT-1996; 96US-0030157P.
PR 21-MAR-1997; 97US-00822953.
PR 07-JAN-1998; 98US-00003886.
PR 20-FEB-1998; 98US-00027287.
PR 19-FEB-1998; 98US-0075409P.
PR 11-MAR-1999; 99US-00252656.
PR 04-JUN-1999; 99US-0137457P.
PR 06-JUL-1999; 99US-0142657P.
PR 11-AUG-1999; 99US-0148326P.
PR 02-DEC-1999; 99US-0168380P.
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PR 10-MAR-2000; 2000US-00523323.  
PR 01-MAR-2002; 2002US-0360234P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ebner R, Yu G, Ruben SM, Zhai Y, Ullrich S;  
XX WPI; 2004-201265/19.  
DR  
XX  
XX Isolated apoptosis inducing molecule II polypeptide, useful for treating,  
PT preventing, ameliorating, diagnosing or prognosing autoimmune diseases  
PT such as multiple sclerosis, rheumatoid arthritis, aplastic anemia.  
XX  
XX Example 13; SEQ ID NO 53; 189pp; English.  
XX  
XX The invention relates to apoptosis inducing molecule II (AIM II), a TNF  
CC (tumour necrosis factor)-ligand superfamily member and its corresponding  
CC nucleic acid sequence. The invention is useful for preventing, treating,  
CC ameliorating, diagnosing or prognosing graft versus host disease,  
CC immunodeficiency, cancer, autoimmune diseases such as multiple sclerosis,  
CC type I diabetes, rheumatoid arthritis, primary biliary cirrhosis,  
CC aplastic anaemia, myelodysplasia, systemic lupus erythematosus and  
CC idiopathic thrombocytopenic purpura. It is useful for screening or  
CC identifying compounds capable of enhancing or inhibiting cellular  
CC response induced by AIM II, for inhibiting, blocking or reducing T-cell  
CC activation. AIM II is useful as a molecular weight marker on SDS-PAGE  
CC gels or on gel filtration columns. The present sequence is a cysteine-  
CC rich motif of human TNF receptor (TNFR) family member.  
XX  
XX Sequence 154 AA;  
SQ  
Query Match 17.7%; Score 200.5; DB 8; Length 154;  
Best Local Similarity 29.8%; Pred. No. 1.2e-07;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
Qy 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQA 99  
Db 9 HPQNNISICTKCHKGTLYNDPCPGQDTCRECESGSFTASENHLR-HCLSCSKCRKEM 67  
Qy 100 SQVALENCSAVADTRCGCKPGWFVEEC---QVSCVSSSPFYCQPCDCLCGALHRRHRLICS 156  
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRWSENLFCQ-----FNCSICLN-GTVH-----LSCQ 117  
Qy 157 RRDDTCGTCLPGFVHEHGDGCVSCPTSTLGSCE--RCAAVC 195  
Db 118 EKQNTVCTCHAGFFLENECVSC-----SNCKSLECTKLC 153  
RESULT 13  
ABG74752  
ID ABG74752 standard; protein; 161 AA.  
XX  
XX ABG74752;  
AC  
XX  
XX 14-MAY-2003 (first entry)  
DT  
XX  
XX Human TNF binding protein fragment.  
DE  
XX  
XX TNF; human; tumour necrosis factor; tumour necrosis factor receptor;  
KW TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.  
XX  
XX Homo sapiens.  
OS  
XX EP393438-A.  
FN  
XX  
XX 24-OCT-1990.  
PD  
XX  
XX 06-APR-1990; 90EP-00106624.  
PF  
XX  
XX 21-APR-1989; 89DE-03913101.  
PR  
XX 21-JUN-1989; 89DE-03920282.  
PR  
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
PA

PA (SYND ) SYNERGEN INC.  
XX  
XX Hauptmann R, Himmler A, Maurerfogy I, Stratowa C;  
XX WPI; 1990-321987/43.  
DR  
XX  
XX DNA encoding TNF binding protein and TNF- receptor - used in tumour  
PT treatment and to understand mechanisms to TNF action.  
PT  
XX  
XX Claim 23; Page 34; 51pp; German.  
PS  
XX  
XX This invention describes novel polynucleotide sequences encoding tumour  
CC necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).  
CC The products of the invention are useful in pharmaceutical compositions  
CC for prophylaxis or treatment of human tumours and to understand the  
CC mechanisms of TNF action. This sequence represents a fragment of the TNF-  
CC BP described in the disclosure of the invention  
XX  
XX Sequence 161 AA;  
SQ  
Query Match 17.7%; Score 200.5; DB 2; Length 161;  
Best Local Similarity 29.8%; Pred. No. 1.2e-07;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
Qy 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQA 99  
Db 11 HPQNNISICTKCHKGTLYNDPCPGQDTCRECESGSFTASENHLR-HCLSCSKCRKEM 69  
Qy 100 SQVALENCSAVADTRCGCKPGWFVEEC---QVSCVSSSPFYCQPCDCLCGALHRRHRLICS 156  
Db 70 GQVEISSCTVDRDTCVCGCRKNQYRWSENLFCQ-----FNCSICLN-GTVH-----LSCQ 119  
Qy 157 RRDDTCGTCLPGFVHEHGDGCVSCPTSTLGSCE--RCAAVC 195  
Db 120 EKQNTVCTCHAGFFLENECVSC-----SNCKSLECTKLC 155  
RESULT 14  
AAR27496  
ID AAR27496 standard; protein; 161 AA.  
XX  
XX AAR27496;  
AC  
XX  
XX 25-MAR-2003 (revised)  
DT  
XX 09-MAR-1993 (first entry)  
DT  
XX  
XX Native 30 kD TNF inhibitor.  
DE  
XX  
XX Tumour necrosis factor; ethylene glycol; pharmacokinetic;  
KW adult respiratory distress syndrome; rheumatoid arthritis; septic shock;  
KW pulmonary fibrosis; spacer.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W09216221-A1.  
FN  
XX  
XX 01-OCT-1992.  
PD  
XX  
XX 13-MAR-1992; 92WO-US002122.  
PF  
XX  
XX 15-MAR-1991; 91US-00669862.  
PR  
XX 17-JAN-1992; 92US-00822296.  
PR  
XX  
XX (SYND ) SYNERGEN INC.  
PA  
XX  
XX Thompson RC, Armes LG, Evans RJ, Brewer MT, Kohno T;  
XX WPI; 1992-348933/42.  
XX  
XX New ethylene glycolated polypeptide(s) with improved pharmacokinetic  
PT properties - for treating e.g. TNF and IL-1 mediated diseases, e.g. adult  
PT respiratory distress syndrome, rheumatoid arthritis, septic shock etc.  
XX

PS Claim 54; Fig 2; 100pp; English.

XX The sequence shows a native 30 kD TNF inhibitor which may be modified to contain at least one non-native cysteine residue, pref. at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such TNF inhibitor moles may be linked via this non-peptidic spacer. The modified polypeptides show improved pharmacokinetic properties, i.e. increased mol. wt. hence reduced clearance rate following s.c. or systemic administration, increased sol. of native TNF inhibitors, and reduced antigenicity. The polypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic shock. The same method may be applied to the interleukin-1 receptor antagonist IL-1ra. See also AAR27495. (Updated on 25-MAR-2003 to correct CC PN field.)

XX SQ Sequence 161 AA;

Query Match 17.7%; Score 200.5; DB 2; Length 161;  
Best Local Similarity 29.8%; Pred. No. 1.2e-07;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQA 99  
DB 11 HPQNNISICTKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKKEM 69

QY 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCLS 156  
DB 70 GQVEISSCTVDRDTCGCRKNQYRHWYSENLFQC-----FNCSLCLN-GTVH----LSCQ 119

QY 157 RRDTCGTCCLPGFYEHGDCVSCPTSTILGSCPE--RCAAVC 195  
DB 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLLECTKLC 155

RESULT 15  
AAW59664  
ID AAW59664 standard; protein; 161 AA.  
AC AAW59664;  
XX  
XX 28-SEP-1998 (first entry)  
XX Human soluble tumour necrosis factor receptor type I.  
XX Human; tumour necrosis factor; TNF; TNF receptor type I;  
KW inflammatory disease; leukaemia; TNF binding protein;  
KW anti-inflammatory drug; methotrexates.  
XX Homo sapiens.  
OS  
XX  
XX WO9824463-A2.  
XX  
XX 11-JUN-1998.  
XX  
XX 08-DEC-1997; 97WO-US022733.  
XX  
XX 06-DEC-1996; 96US-0032587P.  
PR 23-JAN-1997; 97US-0036355P.  
PR 07-FEB-1997; 97US-0039315P.  
PR 09-JUL-1997; 97US-0052023P.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Bendele AM, Sennello RM, Edwards CK;  
XX  
XX WPI; 1998-333039/29.  
DR N-PSDB; AAV41548.  
XX  
XX Treatment of acute or chronic inflammatory disease, e.g. leukaemia - by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.  
PT

XX PS Disclosure; Fig 1; 104pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor receptor type I, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate

XX SQ Sequence 161 AA;

Query Match 17.7%; Score 200.5; DB 2; Length 161;  
Best Local Similarity 29.8%; Pred. No. 1.2e-07;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQA 99  
DB 11 HPQNNISICTKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKKEM 69

QY 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCLS 156  
DB 70 GQVEISSCTVDRDTCGCRKNQYRHWYSENLFQC-----FNCSLCLN-GTVH----LSCQ 119

QY 157 RRDTCGTCCLPGFYEHGDCVSCPTSTILGSCPE--RCAAVC 195  
DB 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLLECTKLC 155

Search completed: June 27, 2005, 14:02:08  
Job time : 164 secs

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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:02:25 ; Search time 162 Seconds  
(without alignments)  
462.882 Million cell updates/sec

Title: US-10-081-280-6\_COPY\_1\_195

Perfect score: 1130

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Maximum DB seq length: 195

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1051	93.0	181	9	US-09-884-733-1
2	1051	93.0	181	9	US-09-993-234-1
3	1051	93.0	181	13	US-10-081-280-1
4	1051	93.0	181	13	US-10-112-793-1
5	1051	93.0	181	14	US-10-112-793-1
6	1051	93.0	188	15	US-10-415-247-5
7	210.5	18.6	162	9	US-09-798-789-12
8	210.5	18.6	162	14	US-10-218-102-422
9	209.5	18.5	190	9	US-09-899-429A-18
10	205.5	18.2	162	9	US-09-798-789-13
11	205.5	18.2	162	9	US-09-798-789-20
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 5, Appli
					Sequence 12, Appl
					Sequence 422, App
					Sequence 18, Appl
					Sequence 13, Appl
					Sequence 20, Appl

12	205.5	18.2	162	14	US-10-218-102-423	Sequence 423, App
13	205.5	18.2	162	14	US-10-218-102-430	Sequence 430, App
14	205	18.1	173	9	US-09-899-429A-16	Sequence 16, Appl
15	205	18.1	183	9	US-09-899-429A-10	Sequence 10, Appl
16	203.5	18.0	162	9	US-09-798-789-11	Sequence 11, Appl
17	203.5	18.0	162	14	US-10-218-102-421	Sequence 421, App
18	201.5	17.8	162	9	US-09-798-789-19	Sequence 19, Appl
19	201.5	17.8	162	9	US-09-798-789-21	Sequence 21, Appl
20	201.5	17.8	162	14	US-10-218-102-429	Sequence 429, App
21	201.5	17.8	162	14	US-10-218-102-431	Sequence 431, App
22	200.5	17.7	153	9	US-09-800-909-3	Sequence 3, Appli
23	200.5	17.7	153	9	US-09-884-987-4	Sequence 4, Appli
24	200.5	17.7	153	9	US-09-800-908-12	Sequence 12, Appli
25	200.5	17.7	153	15	US-10-423-927-3	Sequence 3, Appli
26	200.5	17.7	153	16	US-10-632-929-12	Sequence 12, Appl
27	200.5	17.7	154	13	US-10-112-793-12	Sequence 12, Appl
28	200.5	17.7	154	15	US-10-375-680-53	Sequence 53, Appl
29	200.5	17.7	161	9	US-09-899-422-4	Sequence 4, Appli
30	200.5	17.7	161	9	US-09-907-283-2	Sequence 2, Appli
31	200.5	17.7	161	9	US-09-898-234-4	Sequence 4, Appli
32	200.5	17.7	161	9	US-09-899-429A-4	Sequence 4, Appli
33	200.5	17.7	161	9	US-09-792-356-4	Sequence 4, Appli
34	200.5	17.7	161	10	US-09-882-735-2	Sequence 2, Appli
35	200.5	17.7	161	14	US-10-436-826-73	Sequence 73, Appl
36	200.5	17.7	161	15	US-10-621-783-2	Sequence 2, Appli
37	200.5	17.7	161	15	US-10-622-383-2	Sequence 2, Appli
38	200.5	17.7	161	17	US-10-496-218-1	Sequence 1, Appli
39	200.5	17.7	162	9	US-09-798-789-9	Sequence 9, Appli
40	200.5	17.7	162	9	US-09-798-789-14	Sequence 14, Appl
41	200.5	17.7	162	9	US-09-798-789-22	Sequence 22, Appl
42	200.5	17.7	162	9	US-09-899-429A-6	Sequence 6, Appli
43	200.5	17.7	162	14	US-10-218-102-419	Sequence 419, App
44	200.5	17.7	162	14	US-10-218-102-424	Sequence 424, App
45	200.5	17.7	162	14	US-10-218-102-432	Sequence 432, App

ALIGNMENTS

RESULT 1  
US-09-884-733-1  
; Sequence 1, Application US/09884733  
; Patent No. US20020123116A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 Ligand Inhibitor  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/884,733  
; FILING DATE: 19-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/304,003  
; FILING DATE: 14-JUNE-2000  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5416  
; TELEFAX: 415/952-9881  
;

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TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-884-733-1

Query Match          93.0%; Score 1051; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.8e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCSSAVADTRCGCKPG 120

QY 121 WFEVCQSQCVSSSPFFYCQPCDCLDGCALHRRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
DB 121 WFEVCQSQCVSSSPFFYCQPCDCLDGCALHRRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180

QY 181 T 181
DB 181 T 181

RESULT 2
US-09-993-234-1
; Sequence 1, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,234
; FILING DATE: 19-No. US20020146768A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-993-234-1
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Query Match          93.0%; Score 1051; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.8e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 T 181
DB 181 T 181

RESULT 3
US-10-081-280-1
; Sequence 1, Application US/10081280
; Publication No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,270
; FILING DATE: 31-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-081-280-1

Query Match          93.0%; Score 1051; DB 13; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.8e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 T 181

## RESULT 4

US-10-112-793-1  
; Sequence 1, Application US/10112793  
; Publication No. US2002019279A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/112,793  
; FILING DATE: 28-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,683A  
; FILING DATE: 31-Mar-1997  
; APPLICATION NUMBER: 08/625328  
; FILING DATE: 1-Apr-1996  
; APPLICATION NUMBER: 08/710802  
; FILING DATE: 23-Sep-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1007P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 181 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-112-793-1

Query Match 93.0%; Score 1051; DB 13; Length 181;  
Best Local Similarity 100.0%; Pred. No. 5.8e-76;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120  
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Qy 121 WFVEQVQSQVSSPPFYCQPCLDGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180  
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Qy 181 T 181  
Db 181 T 181

## RESULT 5

US-10-112-193-1  
; Sequence 1, Application US/10112193  
; Publication No. US20030004313A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/112,193  
; FILING DATE: 28-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/928,069  
; FILING DATE: 11-Sep-1997  
; APPLICATION NUMBER: 60/026943  
; FILING DATE: 23-Sep-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1052R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 181 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-112-193-1

Query Match 93.0%; Score 1051; DB 14; Length 181;  
Best Local Similarity 100.0%; Pred. No. 5.8e-76;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEQPRGCAAVAAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120  
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120  
Qy 121 WFVEQVQSQVSSPPFYCQPCLDGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180  
Db 121 WFVEQVQSQVSSPPFYCQPCLDGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180  
Qy 181 T 181  
Db 181 T 181

## RESULT 6

US-10-415-247-5



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; Sequence 5, Application US/10415247
; Publication No. US20040013655A1
; GENERAL INFORMATION:
; APPLICANT: Shiozawa, Shunichi
; TITLE OF INVENTION: Genome responsible for chronic rheumatoid arthritis,
; TITLE OF INVENTION: diagnostic method, pathogenicity judging method and
; TITLE OF INVENTION: detection-use diagnostic kit of chronic rheumatoid
; TITLE OF INVENTION: arthritis, and therapeutic method and medicine of
; TITLE OF INVENTION: chronic rheumatoid arthritis
; FILE REFERENCE: TLOPI-2
; CURRENT APPLICATION NUMBER: US/10/415,247
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: JP 2000-324296
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: JP 2001-90546
; PRIOR FILING DATE: 2001-3-27
; PRIOR APPLICATION NUMBER: JP 2001-99990
; PRIOR FILING DATE: 2001-3-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-247-5

Query Match      93.0%; Score 1051; DB 15; Length 188;
Best Local Similarity 100.0%; Pred. No. 5.9e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAAAVALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAAVALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCSAVADTRCGCKPG 120

Qy 121 WFEVCQSVQCVSSSPFYCQPCLDGALHRRHRLICSRDTCGTCPLGFGYEHGDCVSCP 180
Db 121 WFEVCQSVQCVSSSPFYCQPCLDGALHRRHRLICSRDTCGTCPLGFGYEHGDCVSCP 180

Qy 181 T 181
Db 181 T 181

RESULT 7
US-09-798-789-12
; Sequence 12, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-12

Query Match      18.6%; Score 210.5; DB 9; Length 162;
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Best Local Similarity 30.0%; Pred. No. 3.4e-09;
Matches 48; Conservative 20; Mismatches 73; Indels 19; Gaps 6;

Qy 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQA 99
Db 12 HPQNNISICCTKCHKGTLYNDPCPGQDTCRECESGSFTASE-EHKRECLRCRCRDKM 70

Qy 100 SOVALENCNSAVADTRCGCKPGWFEVCQSVQCVSSSPFYCQPCLDG--GALHRRHRLICSR 157
Db 71 GQVEISSCTVDRDVTVCGRKN-----QYRHYETENEFFCFNCSLCNLGTVH----LSCQE 121

Qy 158 RDTDCGTCLPGFYEHGDCVSCPTSTILGSCPE--RCAAVC 195
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 8
US-10-218-102-422
; Sequence 422, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 09/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/352,103
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 422
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-218-102-422

Query Match      18.6%; Score 210.5; DB 14; Length 162;
Best Local Similarity 30.0%; Pred. No. 3.4e-09;
Matches 48; Conservative 20; Mismatches 73; Indels 19; Gaps 6;

Qy 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQA 99
Db 12 HPQNNISICCTKCHKGTLYNDPCPGQDTCRECESGSFTASE-EHKRECLRCRCRDKM 70

Qy 100 SOVALENCNSAVADTRCGCKPGWFEVCQSVQCVSSSPFYCQPCLDG--GALHRRHRLICSR 157
Db 71 GQVEISSCTVDRDVTVCGRKN-----QYRHYETENEFFCFNCSLCNLGTVH----LSCQE 121

Qy 158 RDTDCGTCLPGFYEHGDCVSCPTSTILGSCPE--RCAAVC 195
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 9
US-09-899-429A-18
; Sequence 18, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
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; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1955-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-BP sequence
US-09-899-429A-18

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Query Match	18.5%;	Score	209.5;	DB	9;	Length	190;
Best Local Similarity	29.0%;	Pred. NO.	4.7e-09;				
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						Gaps	7;
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Db	15	LLELLVGIYSGVIGDSV	CP	GKGIYHPNNIS	ICCTKHKGTYLYND	CGPGQDTCRGE	74
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Qy	75	QDTFLAVENHHNSCAR	COA	CDEQASQVALN	SCSAVATRCGCKRPGWPEC	---QVSQCV	131
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Db	75	SGSPFASENHLR	-HCL	SCSKCRKEMGQVEI	SSCTVDRTVCGCRKNQRYHMYSENLP	QC-	132
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Qy	132	SSSPFYCQPCLCDGAL	HRHTLL	CGSRDRDTCG	TCLPGFYEHGDCGVC	SCPTSLGSCPE-	189
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Qy	190	RCAAVC	195				
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Db	179	ECTKLC	184				
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RESULT 10
US-09-798-789-13
; Sequence 13, Application US/09798789
; Patent No. US2002009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahivat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 13
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-13

Query Match      18.2%; Score 205.5; DB 9; Length 162;
Best Local Similarity 30.0%; Pred. No. 8.5e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19; Gaps 6

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Db 12 HPQNNISICTKCHKRGTYLYNDPCPGQDTCRECESGSFTASENHLR-DLQCQCCKKH 70
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Qy 100 SOVALENCASAVDRTCGCKPGWFECQVSCQVSSPFYCPCLDC--GALHRRHTLLCSR 157
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Db 71 GQVTSISCTVDRDTCGGRKN-----QYRHYDHNRFYCFNCSCLNGTVH----LSQCE 121

Qy 158 RDTDCGTCLPGFYEHGDCGVSCPTSTLGSQPE--RCAAVC 195

Db 122 KONTVCTCHAGFFLRENECVS-----SNCKKSLCTKLC 156

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RESULT 11
; US-09-798-789-20
; Sequence 20, Application US/0798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-798-789-20

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Query Match	18.2%	Score	205.5	DB	9	Length	162
Best Local Similarity	30.4%	Prod. No.	8.5e-09				
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						Gaps	7
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Db	12	HPQNNISCCCTKCHGTGYLDNCPGGQDTCRECSGFTASENHLR-HCLSCSKCRKEM	70				
Qy	100	SQVALENGSAVADTRCGCKPGWFVECQ---VSQCVSSPPFYCQPLCDGCALHRHTRLLCS	156				
Db	71	GOVEISSCTVDRTVCGCRKNQRYHQSENLFQC-----FNCSLCLN-GTVH-----LSCQ	120				
Qy	157	RRDTRDGTGCLPGFVHGHDGVCVSPCTSTLGSQPE--RCAAVC	195				
Db	121	EKONTVCTCHAGFFLENECVSC-----SNCKKSLECTKLC	156				

RESULT 12  
US-10-218-423  
; Sequence 423, Application US/10218102  
; Publication No. US20030130827A1  
; GENERAL INFORMATION:  
; APPLICANT: Benzien, Joerg  
; APPLICANT: Dahiyat, Basil I.  
; APPLICANT: Desjarlats, John R.  
; APPLICANT: Hayes, Robert J.  
; APPLICANT: Vielmetter, Jost



Db 162 ECTKLC 167

RESULT 15  
US-09-899-429A-10  
; Sequence 10, Application US/09899429A  
; Patent No. US20020169118A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmeler, Adolph  
; APPLICANT: Maurer-Poggy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; FILE REFERENCE: 98-385-J  
; CURRENT APPLICATION NUMBER: US/09/899,429A  
; PRIOR FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/792,356  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 08/477,639  
; PRIOR FILING DATE: 1955-06-07  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: Patentin ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recombinant  
; OTHER INFORMATION: TNF-BP sequence  
US-09-899-429A-10

Query Match 18.1%; Score 205; DB 9; Length 183;  
Best Local Similarity 29.0%; Pred.No.1e-08;  
Matches 54; Conservative 23; Mismatches 85; Indels 24; Gaps 8;  
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Db 1 MLVPHLGDRK--RDSVCPQGYIHPQNNISCTCKCHKGYLYNDGCPGQDTCRECE 57  
Qy 75 QDTFLAWENHNSECARCOAQDEQASQVALENCSAVADTRCGCKPGWFVEC---QVSQCV 131  
Db 58 SGSEFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHYWSENLFQC- 115  
Qy 132 SSSPFYCPCLDCGALHRRHTLLCSRRDTCGTCLPGFYEHDGCVSCPTLGCSPB-- 189  
Db 116 ----FNCSLCLN-GTVH----LSCQEKQNTVCTCHAGFFLENECVSC-----SNCKKSL 161  
Qy 190 RCAAVC 195  
Db 162 ECTKLC 167

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2005, 13:53:44 ; Search time 42 Seconds  
(without alignments)  
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Title: US-10-081-280-6\_COPY\_1\_195  
Perfect score: 1130  
Sequence: 1 MEQPRGCAVAALLLVLL.....CVSCPTSLGSCPRCAAVC 195

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 390715

Minimum DB seq length: 0  
Maximum DB seq length: 195

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1051	93.0	181	4	US-08-828-683A-1
3	200.5	17.7	153	2	US-08-213-237B-4
4	200.5	17.7	153	3	US-08-477-347-12
5	200.5	17.7	153	3	US-08-476-862-3
6	200.5	17.7	153	3	US-08-468-560C-4
7	200.5	17.7	153	4	US-09-800-909-3
8	200.5	17.7	153	4	US-09-800-908-12
9	200.5	17.7	154	4	US-08-828-683A-12
10	200.5	17.7	154	4	US-09-523-323-53
11	200.5	17.7	161	3	US-09-326-394-2
12	198.5	17.6	154	2	US-08-232-087A-10
13	196	17.3	139	3	US-08-706-945D-129
14	191	16.9	181	4	US-09-513-007-4
15	186	16.5	193	3	US-09-146-950-2
16	185	16.4	123	4	US-09-855-266A-13
17	182	16.1	155	3	US-09-146-950-4
18	182	16.1	159	3	US-09-146-950-20
19	175.5	15.5	158	1	US-08-050-319B-54
20	175.5	15.5	158	2	US-08-465-982-54
21	174.5	15.4	161	4	US-09-523-323-50
22	171.5	15.2	180	4	US-09-612-033B-10
23	166	14.7	167	1	US-08-050-319B-2
24	166	14.7	167	1	US-08-050-319B-57
25	166	14.7	167	2	US-08-465-982-2
26	166	14.7	167	2	US-08-465-982-57
27	164.5	14.6	148	3	US-09-411-722-2

28	164.5	14.6	148	4	US-09-855-266A-2	Sequence 2, Appli
29	164.5	14.6	176	3	US-09-411-722-1	Sequence 1, Appli
30	164.5	14.6	176	4	US-09-855-266A-1	Sequence 1, Appli
31	162.5	14.4	119	2	US-08-219-237B-3	Sequence 3, Appli
32	162.5	14.4	119	3	US-08-477-347-14	Sequence 14, Appli
33	162.5	14.4	119	3	US-08-476-862-5	Sequence 5, Appli
34	162.5	14.4	119	3	US-08-468-560C-3	Sequence 3, Appli
35	162.5	14.4	119	4	US-08-828-683A-15	Sequence 15, Appli
36	162.5	14.4	119	4	US-09-800-909-5	Sequence 5, Appli
37	162.5	14.4	119	4	US-09-800-908-14	Sequence 14, Appli
38	162.5	14.4	128	3	US-09-180-100-9	Sequence 9, Appli
39	162.5	14.4	143	3	US-09-180-100-10	Sequence 10, Appli
40	162.5	14.4	144	3	US-09-180-100-21	Sequence 21, Appli
41	162.5	14.4	157	3	US-09-180-100-15	Sequence 15, Appli
42	162.5	14.4	159	3	US-09-180-100-23	Sequence 23, Appli
43	162.5	14.4	167	4	US-08-828-683A-22	Sequence 22, Appli
44	158.5	14.0	124	1	US-08-050-319B-4	Sequence 4, Appli
45	158.5	14.0	124	2	US-08-465-982-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-08-928-069-1  
; Sequence 1, Application US/08928069  
; Patent No. 6462176  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,069  
; FILING DATE: 11-Sep-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/026943  
; FILING DATE: 09/23/1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1052R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 181 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-928-069-1

Query Match 93.0%; Score 1051; DB 4; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1.7e-09;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Db 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHSEACRQCACDQASQVALENCASVADTRCGCKPG 120

Db 61 CTEPCGNTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120  
QY 121 WFVECVQSQVSSPPFYCQPCLDGALHRRHRLTLLCSRRDTCGTCCLPGFYEHGDCVSCP 180  
Db 121 WFVECVQSQVSSPPFYCQPCLDGALHRRHRLTLLCSRRDTCGTCCLPGFYEHGDCVSCP 180  
QY 181 T 181  
Db 181 T 181  
RESULT 2  
US-08-828-683A-1  
; Sequence 1, Application US/08828683A  
; Patent No. 6469144  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,683A  
; FILING DATE: 31-Mar-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/625328  
; FILING DATE: 1-Apr-1996  
; APPLICATION NUMBER: 08/710802  
; FILING DATE: 23-Sep-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1007P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 181 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-08-828-683A-1  
Query Match 93.0%; Score 1051; DB 4; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1.7e-89;  
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
Db 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60  
QY 61 CTEPCGNTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120  
Db 61 CTEPCGNTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120  
QY 121 WFVECVQSQVSSPPFYCQPCLDGALHRRHRLTLLCSRRDTCGTCCLPGFYEHGDCVSCP 180  
Db 121 WFVECVQSQVSSPPFYCQPCLDGALHRRHRLTLLCSRRDTCGTCCLPGFYEHGDCVSCP 180  
QY 181 T 181

Db 181 T 181  
RESULT 3  
US-08-219-237B-4  
; Sequence 4, Application US/08219237B  
; Patent No. 5874546  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu  
; APPLICANT: ITOH, Naoto  
; APPLICANT: YONEHARA, Shin  
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James W. Hellwege  
; STREET: P.O. Box 2266 Eads Station  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/219,237B  
; FILING DATE: 28-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/872,129  
; FILING DATE: 22-APR-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James W. Hellwege  
; REGISTRATION NUMBER: 28,808  
; REFERENCE/DOCKET NUMBER: 516762  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 153 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-219-237B-4  
Query Match 17.7%; Score 200.5; DB 2; Length 153;  
Best Local Similarity 29.8%; Pred. No. 3.5e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
QY 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNTCLVCPQDTFLAWENHNSECARQACDEQA 99  
Db 9 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 67  
QY 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSCVSSSPFYCQPCLDGALHRRHRLTLLCS 156  
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQC-----FNCSLCLN-GTVH----LSCQ 117  
QY 157 RRDTDCGTCCLPGYEHGDCGVCSTLTGSCPE--RCAAVC 195  
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSELECTKLC 153  
RESULT 4  
US-08-477-347-12  
; Sequence 12, Application US/08477347  
; Patent No. 6232446  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BIGDA, Jacek  
; APPLICANT: BELETSKY, Igor  
; APPLICANT: MEIT, Igor  
; TITLE OF INVENTION: TNF LIGANDS



NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477.347  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/115,685  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 106271  
FILING DATE: 08-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, G. Kevin  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: WALLACH=10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 153 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-347-12

Query Match 17.7%; Score 200.5; DB 3; Length 153;  
Best Local Similarity 29.8%; Pred. No. 3.5e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
QY 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDQA 99  
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QY 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDCLDGCALHRRHRLCS 156  
DB 68 GQVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCLN-GTVH----LSCQ 117  
QY 157 RRDTCGTCCLPGFYEHDGCVSCPTSLGSCPE--RCAAVC 195  
DB 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 153

## RESULT 5

US-08-476-862-3  
Sequence 3, Application US/08476862  
Patent No. 626239  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BIGDA, Jacek  
APPLICANT: BELETSKY, Igor  
APPLICANT: METT, Igor  
APPLICANT: ENGELMANN, Hartmut  
TITLE OF INVENTION: TNF INHIBITORS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W.  
CITY: Washington

STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476.862  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 107267  
FILING DATE: 12-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 94039  
FILING DATE: 06-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 91229  
FILING DATE: 06-AUG-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 90339  
FILING DATE: 18-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=12A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 153 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-476-862-3

Query Match 17.7%; Score 200.5; DB 3; Length 153;  
Best Local Similarity 29.8%; Pred. No. 3.5e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
QY 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDQA 99  
DB 9 HPQNNISICTKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 67  
QY 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDCLDGCALHRRHRLCS 156  
DB 68 GQVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCLN-GTVH----LSCQ 117  
QY 157 RRDTCGTCCLPGFYEHDGCVSCPTSLGSCPE--RCAAVC 195  
DB 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 153

## RESULT 6

US-08-468-560C-4  
Sequence 4, Application US/08468560C  
Patent No. 6270998  
GENERAL INFORMATION:  
APPLICANT: NAGATA, Shigekazu  
APPLICANT: ITOH, Naoto  
APPLICANT: YONEHARA, Shin  
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE  
TITLE OF INVENTION: ANTIGEN  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.  
STREET: P.O. BOX 747  
CITY: FALLS CHURCH  
STATE: VA

; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,560C  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR., GERLAD M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 20-4393P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-205-8000  
; TELEFAX: 703-205-8050  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 153 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-468-560C-4

Query Match 17.7%; Score 200.5; DB 3; Length 153;  
Best Local Similarity 29.8%; Pred. No. 3.5e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
  
Qy 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSGTCVCPQDTFLAWENHNHNSCARCOACDEQA 99  
Db 9 HPQNSICCTCKHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 67  
  
Qy 100 SQVALENCASAVATRCGCKPGWFVEC---QVSCQVSSSPFYCQPLDCGALHRRHRLCLS 156  
Db 68 QGVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCLN-GTVH----LSCQ 117  
  
Qy 157 RRDTDCGTCPLGFYEHGDCGVCSTLTGSCPE--RCAAVC 195  
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 153

RESULT 7  
US-800-909-3  
; Sequence 3, Application US/09800909  
; Patent No. 655111  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BIGDA, Jacek  
; APPLICANT: BELETSKY, Igor  
; APPLICANT: METT, Igor  
; APPLICANT: ENGELMANN, Hartmut  
; TITLE OF INVENTION: TNF INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/800,909  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/476,862  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 94039  
; FILING DATE: 06-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 91229  
; FILING DATE: 06-AUG-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 90339  
; FILING DATE: 18-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH-12A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 153 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-800-909-3

Query Match 17.7%; Score 200.5; DB 4; Length 153;  
Best Local Similarity 29.8%; Pred. No. 3.5e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
  
Qy 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSGTCVCPQDTFLAWENHNHNSCARCOACDEQA 99  
Db 9 HPQNSICCTCKHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 67  
  
Qy 100 SQVALENCASAVATRCGCKPGWFVEC---QVSCQVSSSPFYCQPLDCGALHRRHRLCLS 156  
Db 68 QGVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCLN-GTVH----LSCQ 117  
  
Qy 157 RRDTDCGTCPLGFYEHGDCGVCSTLTGSCPE--RCAAVC 195  
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 153

RESULT 8  
US-09-800-908-12  
; Sequence 12, Application US/09800908  
; Patent No. 6602993  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BIGDA, Jacek  
; APPLICANT: BELETSKY, Igor  
; APPLICANT: METT, Igor  
; TITLE OF INVENTION: TNF LIGANDS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/800,908  
; FILING DATE: 08-Mar-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/477,347

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; FILING DATE: <Unknown>
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-800-908-12

      Query Match      17.7%; Score 200.5; DB 4; Length 153;
      Best Local Similarity 29.8%; Pred. No. 3.5e-11;
      Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 40 HKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNHSECARCQACDQA 99
Db 9 HPQNNISCTCKHKGTYLNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCKEM 67

QY 100 SOVALENCASAVADTRCGCKPGWFVFC-----QVSQCVSSPPFYCQCLDGCALHRRHRLCS 156
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQC-----FNCSLCIN-GTVH----LSCQ 117

QY 157 RRDTDCGTCLPGFVEHGDGVCSTPTSLGSCPE--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 153

      RESULT 9
      US-08-828-683A-12
      ; Sequence 12, Application US/08828683A
      ; Patent No. 6469144
      ; GENERAL INFORMATION:
      ; APPLICANT: Ashkenazi, Avi J.
      ; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
      ; NUMBER OF SEQUENCES: 28
      ; CORRESPONDENCE ADDRESS:
      ; ADDRESSEE: Genentech, Inc.
      ; STREET: 1 DNA Way
      ; CITY: South San Francisco
      ; STATE: California
      ; COUNTRY: USA
      ; ZIP: 94080
      ; COMPUTER READABLE FORM:
      ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
      ; COMPUTER: IBM PC compatible
      ; OPERATING SYSTEM: PC-DOS/MS-DOS
      ; SOFTWARE: Winpatin (Genentech)
      ; CURRENT APPLICATION DATA:
      ; APPLICATION NUMBER: US/08/828,683A
      ; FILING DATE: 31-Mar-1997
      ; CLASSIFICATION: <Unknown>
      ; PRIOR APPLICATION DATA:
      ; APPLICATION NUMBER: 08/625328
      ; FILING DATE: 1-Apr-1996
      ; APPLICATION NUMBER: 08/710802
      ; FILING DATE: 23-Sep-1996
      ; ATTORNEY/AGENT INFORMATION:
      ; NAME: Marschang, Diane L.
      ; REGISTRATION NUMBER: 35,600
      ; REFERENCE/DOCKET NUMBER: P1007P1
      ; TELECOMMUNICATION INFORMATION:
      ; TELEPHONE: 650/225-5416
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; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-828-683A-12

      Query Match      17.7%; Score 200.5; DB 4; Length 154;
      Best Local Similarity 29.8%; Pred. No. 3.5e-11;
      Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 40 HKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNHSECARCQACDQA 99
Db 9 HPQNNISCTCKHKGTYLNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCKEM 67

QY 100 SOVALENCASAVADTRCGCKPGWFVFC-----QVSQCVSSPPFYCQCLDGCALHRRHRLCS 156
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQC-----FNCSLCIN-GTVH----LSCQ 117

QY 157 RRDTDCGTCLPGFVEHGDGVCSTPTSLGSCPE--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 153

      RESULT 10
      US-09-523-323-53
      ; Sequence 53, Application US/09523323
      ; Patent No. 6635743
      ; GENERAL INFORMATION:
      ; APPLICANT: Ebner, Reinhard
      ; APPLICANT: Yu, Guo-Liang
      ; APPLICANT: Ruben, Steven M.
      ; APPLICANT: Ullrich, Stephen
      ; APPLICANT: Zhai, Yifan
      ; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
      ; FILE REFERENCE: 1488.065000C
      ; CURRENT APPLICATION NUMBER: US/09/523,323
      ; CURRENT FILING DATE: 2000-03-10
      ; EARLIER APPLICATION NUMBER: 60/168,380
      ; EARLIER FILING DATE: 1999-12-02
      ; EARLIER APPLICATION NUMBER: 60/148,326
      ; EARLIER FILING DATE: 1999-08-11
      ; EARLIER APPLICATION NUMBER: 60/142,657
      ; EARLIER FILING DATE: 1999-07-06
      ; EARLIER APPLICATION NUMBER: 60/137,457
      ; EARLIER FILING DATE: 1999-06-04
      ; EARLIER APPLICATION NUMBER: 60/124,041
      ; EARLIER FILING DATE: 1999-03-11
      ; EARLIER APPLICATION NUMBER: 09/252,656
      ; EARLIER FILING DATE: 1999-02-19
      ; EARLIER APPLICATION NUMBER: 60/075,409
      ; EARLIER FILING DATE: 1998-02-20
      ; EARLIER APPLICATION NUMBER: 09/027,287
      ; EARLIER FILING DATE: 1998-02-20
      ; EARLIER APPLICATION NUMBER: 09/003,886
      ; EARLIER FILING DATE: 1998-01-07
      ; EARLIER APPLICATION NUMBER: 08/822,953
      ; EARLIER FILING DATE: 1997-03-21
      ; EARLIER APPLICATION NUMBER: 60/013,923
      ; EARLIER FILING DATE: 1996-03-22
      ; EARLIER APPLICATION NUMBER: 60/030,157
      ; EARLIER FILING DATE: 1996-10-31
      ; NUMBER OF SEQ ID NOS: 70
      ; SOFTWARE: Patentin Ver. 2.0
      ; SEQ ID NO 53
      ; LENGTH: 154
      ; TYPE: PRT
      ; ORGANISM: Homo sapiens
      ; US-09-523-323-53

      Query Match      17.7%; Score 200.5; DB 4; Length 154;
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Best Local Similarity 29.8%; Pred. No. 3.5e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 40 HKKIGLFCRCGPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNHSECARCOACDEQA 99  
Db 9 HPQNNISICTCKCHKGTLYNDPCPGQDTCRECESGFTASENHLR-HCLSCSKCRKEM 67  
Qy 100 SQALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQCLDCGALHRRHRLTLC 156  
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFCQ-----FNCSLCLN-GTVH-----LSCQ 117

Qy 157 RRDTCGTCPLPGFVEHGDGCVSCPTSTLGSCE--RCAAVC 195  
Db 118 EKQNTVCTCHAGFFLENECVSC-----SNCKSLECTKLC 153

RESULT 11  
US-09-326-394-2  
; Sequence 2, Application US/09326394  
; Patent No. 6306820  
; GENERAL INFORMATION:  
; APPLICANT: Bendele, Alison M.  
; APPLICANT: Sennello, Regina M.  
; APPLICANT: Edwards, Carl K.  
; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING  
; TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/09/326,394  
; APPLICATION NUMBER: US/09/326,394  
; FILING DATE: 08-DEC-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/032,587  
; FILING DATE: 06-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,355  
; FILING DATE: 23-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/039,315  
; FILING DATE: 07-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/052,023  
; FILING DATE: 09-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zindrick, Thomas K.  
; REGISTRATION NUMBER: 32,185  
; REFERENCE/DOCKET NUMBER: A-430D  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 161 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-326-394-2

Query Match 17.7%; Score 200.5; DB 3; Length 161;  
Best Local Similarity 29.8%; Pred. No. 3.7e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 40 HKKIGLFCRCGPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNHSECARCOACDEQA 99  
Db 48 GQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFCQ-----FNCSLCLN-GTVH-----LSCQ 117

Db 11 HPQNNISICTCKCHKGTLYNDPCPGQDTCRECESGFTASENHLR-HCLSCSKCRKEM 69  
Qy 100 SQALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQCLDCGALHRRHRLTLC 156  
Db 70 GQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFCQ-----FNCSLCLN-GTVH-----LSCQ 119  
Qy 157 RRDTCGTCPLPGFVEHGDGCVSCPTSTLGSCE--RCAAVC 195  
Db 120 EKQNTVCTCHAGFFLENECVSC-----SNCKSLECTKLC 155

RESULT 12  
US-08-232-087A-10  
; Sequence 10, Application US/08232087A  
; Patent No. 5866372  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Harald  
; APPLICANT: Dtkop, Horst  
; APPLICANT: Latza, Ute  
; TITLE OF INVENTION: Lymphoid CD30-Antigen  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: 8110 Gatehouse Road, Suite 500 East  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22042  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/232,087A  
; APPLICATION NUMBER: US/08/232,087A  
; FILING DATE: 08-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy Jr., Gerald M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 756-103P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 154 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..154  
; OTHER INFORMATION: /note= "TNFRL, see Fig. 5"  
US-08-232-087A-10

Query Match 17.6%; Score 198.5; DB 2; Length 154;  
Best Local Similarity 30.4%; Pred. No. 5.4e-11;  
Matches 49; Conservative 23; Mismatches 68; Indels 21; Gaps 8;

Qy 40 HKKIGLFCRCGPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNHSECARCOACDEQA 99  
Db 9 HPQNNISICTCKCHKGTLYNDPCPGQDTCRECESGFTASENHLR-HCLSCSKCRKEM 67  
Qy 100 SQALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQCLDCGALHRRHRLTLC 156  
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFCQ-----FNCSLCLN-GTVHLSGQ---E 118  
Qy 157 RRDTCGTCPLPGFVEHGDGCVSCPTSTLGSCE--RCAAVC 195

QY 40 HKKIGLFCRCRGPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99

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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:04:00 ; Search time 38 Seconds  
(without alignments)  
440.571 Million cell updates/sec

Title: US-10-081-280-6\_COPY\_25\_198

Perfect score: 1038

Sequence: 1 QGTRSPRCDGDFHKKIG.....CPTSTLGSPCRCAAVCGWR 174

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Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 87400

Minimum DB seq length: 0

Maximum DB seq length: 174

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	96.5	9.3	141	2 PC1294	trophozoite surfac
3	96	9.2	149	2 S58662	Fas-Delta-(4,7) pr
4	94.5	9.1	104	2 S50911	metallothionein-2
5	93.5	9.0	143	2 B21761	high cysteine chor
6	90	8.7	126	2 I46489	cysteine-rich hair
7	88	8.5	167	1 AG0369	ferredoxin-type pr
8	86	8.3	151	2 S60314	hair keratin cyste
9	84.5	8.1	168	2 S06570	finger protein (cl
10	83.5	8.0	131	1 KRGT3M	keratin high-sulfu
11	83.5	8.0	152	2 I47108	high-sulfur wool m
12	83.5	8.0	171	2 I48298	cellular nucleic a
13	83	8.0	170	2 A55499	zinc finger protei
14	83	8.0	170	2 I48297	cellular nucleic a
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16	82	7.9	130	1 KRSH3A	keratin high-sulfu
17	81.5	7.9	164	2 T24272	hypothetical prote
18	80.5	7.8	163	2 F65072	hypothetical prote
19	80	7.7	157	2 G65156	Putative electron
20	80	7.7	160	2 T25185	hypothetical prote
21	79.5	7.7	157	2 F86032	hypothetical prote
22	79.5	7.7	157	2 H91185	hypothetical prote
23	79.5	7.7	168	1 B82430	iron-sulfur cluste
24	79	7.6	132	2 T20463	hypothetical prote
25	78.5	7.6	92	2 D37057	epithelial cell gl
26	78	7.5	79	2 E83378	probable metalloth
27	78	7.5	152	1 KRSHHC	keratin high-sulfu
28	78	7.5	152	2 I47111	high-sulfur wool m
29	78	7.5	155	2 B32669	vasotocin 2 / neur

30	77.5	7.5	68	2 S44392	metallothionein 3
31	77	7.4	85	2 T07090	metallothionein-II
32	77	7.4	132	1 KRGT3J	keratin high-sulfu
33	76.5	7.4	68	2 JC6521	metallothionein II
34	76	7.3	131	2 F91098	probable oxidoredu
35	76	7.3	131	2 B85944	probable oxidoredu
36	76	7.3	135	2 T15610	hypothetical prote
37	75.5	7.3	166	1 D95346	NapH Ferrredoxin co
38	75	7.2	69	2 A55011	metallothionein-II
39	75	7.2	85	2 T05719	metallothionein II
40	75	7.2	166	2 H75154	electron transport
41	75	7.2	168	2 S06557	finger protein (cl
42	74.5	7.2	68	2 I67866	growth inhibitory
43	74.5	7.2	68	2 A46034	metallothionein 3,
44	74.5	7.2	124	2 A21761	high-cysteine chor
45	74.5	7.2	153	2 B83410	probable oxidoredu

ALIGNMENTS

RESULT 1

S18946

ultra high-sulfur keratin 1 - human

N:Alternate names: UHS keratin; ultra high-sulfur matrix protein

C:Species: Homo sapiens (man)

C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004

C:Accession: S18946; B36686

R:Drabant, B.; Doenecke, D.

submitted to the EMBL Data Library, December 1991

A:Description: Nucleotide sequence of a Human high-sulphur keratin cDNA.

A:Reference number: S18946

A:Accession: S18946

A:Molecule type: mRNA

A:Residues: 1-169 <DRA>

A:Cross-references: UNIPROT:Q14564; EMBL:X63755; NID:g32471; PIDN:CAA45283.1; PID:g32472

R:MacKinnon, P.J.; Powell, B.C.; Rogers, G.E.

J. Cell Biol. 111, 2587-2600, 1990

A:Title: Structure and expression of genes for a class of cysteine-rich proteins of the c

A:Reference number: A36686; MUID:91115951; PMID:1703541

A:Accession: B36686

A:Molecule type: DNA

A:Residues: 1-39, 'Y', 41-169 <MAC>

A:Cross-references: GB:X55293; NID:g34078; PIDN:CAA39005.1; PID:g34079

C:Genetics:

A:Gene: GDB:KRN1

A:Cross-references: GDB:I25257; OMIM:148021

A:Map position: 11q13-11q13

C:Superfamily: ultra-high-sulfur keratin

C:Keywords: hair; tandem repeat

F:7-15/Region: Ser-rich nonapeptide repeat

F:59-68/Region: Gly-rich decapeptide repeat

F:69-78/Region: Gly-rich decapeptide repeat

F:79-88/Region: Cys-rich decapeptide repeat

F:89-97/Region: Ser-rich nonapeptide repeat

F:98-107/Region: Cys-rich decapeptide repeat

F:108-117/Region: Cys-rich nonapeptide repeat

F:118-126/Region: Ser-rich nonapeptide repeat

F:127-136/Region: Cys-rich decapeptide repeat

F:137-145/Region: Ser-rich nonapeptide repeat

F:146-155/Region: Cys-rich decapeptide repeat

F:156-165/Region: Cys-rich decapeptide repeat

Query Match '9.9%; Score 103; DB 1; Length 169;

Best Local Similarity 25.3%; Pred. No. 0.58;

Matches 45; Conservative 6; Mismatches 71; Indels 56; Gaps 12;

QY 23 CCRGCPAGHYLKAPCTEPCG--NSTCLVCPQDTFLAMENHNSCARCQ-----ACD 72

Db 3 CC-GCSGG-----CGSSCGGCDSSCGSC-----GSGCRGGGPPSCAPVCCCK 43

QY 73 EQASQVALENCASAVADTRCG-C--KPGWFVFCQVSSSPFFVC-----QBCLDCGALH 124



Db 44 PVCCVPAACSSCGKRGCGSGKGGCGSCGSCCKPCCGSSGCGSCCQCSC-- 101

QY 125 RHTRLLCSRRDDTCGLPGFYEHGSG---CVS-----CPTSTLGS--CPCRCAAVC 171

Db 102 -----CRPYCQCSCCKPCCSSSGSGSCCQSSCKPCPCSSSGCGSCCCKPC 153

RESULT 2

PC1294

C:Species: Giardia lamblia

C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004

C:Accession: PC1294

R:Etymology: P.L.; Mayrhofer, G.

Gene 129, 257-262, 1993

A:Title: Two genes encoding homologous 70-kDa surface proteins are present within individual Giardia lamblia

A:Reference number: PC1294; MUID:93314970; PMID:8325510

A:Accession: PC1294

A:Molecule type: DNA

A:Residues: 1-141 <EYP>

C:Genetics: ts

A:Gene: ts

C:Keywords: surface antigen

Query Match 9.3%; Score 96.5; DB 2; Length 141;

Best Local Similarity 27.2%; Pred. No. 1.5;

Matches 41; Conservative 10; Mismatches 65; Indels 35; Gaps 9;

QY 42 GNSTCLVCPQDTFLAWHHNSECA-----RCQACDEQASQVALENCSSAVADT-----RCG 92

Db 3 GASYSCECATTT-----EYPQNGVCAPKASRATPTCNDSPIQNGV--CGTCADNYFKMNGG 56

QY 93 C-----KPCWFVECVQSVCS-SPFYCQPCLCDGALHRRHRLLCGR-----RDTDCGT 140

Db 57 CYETVKYPKTV-----CISAPNGTCKQADGVKLSGLTLVCSGCKSCTSTSDCTT 110

QY 141 CLPGFYEHGDCVSCPTS--TLGSCPCRCAA 169

Db 111 CLDGVKVSASACTKCDSSCEITCNGAATTCKA 141

RESULT 3

S58662

Fas-Delta-(4,7) protein - human

C:Species: Homo sapiens (man)

C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C:Accession: S58662; S57566

R:Liou, C.; Cheng, J.; Mountz, J.D.

Biochem. J. 310, 957-963, 1995

A:Title: Differential expression of human Fas mRNA species upon peripheral blood mononuclear cell activation

A:Reference number: S58662; MUID:96013198; PMID:7575433

A:Accession: S58662

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-149 <LIU>

A:Cross-references: UNIPROT:P25445

R:Schatzlein, C.E.

submitted to the ENBL Data Library, June 1995

A:Reference number: S57566

A:Accession: S57566

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-132 <SCH>

A:Cross-references: EMBL:X89101; NID:g887457; PID:g887458

C:Keywords: alternative splicing

Query Match 9.2%; Score 96; DB 2; Length 149;

Best Local Similarity 33.3%; Pred. No. 1.7;

Matches 18; Conservative 7; Mismatches 29; Indels 0; Gaps 0;

QY 20 GLPCCRGCPCAGHYLKAPCTEPCGNTCLVCPQDTFLAWHHNSECARCQACDE 73

Db 56 GQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRRCLCDE 109

RESULT 4

S50911

metallothionein-2 - Tetrahymena pigmentosa

C:Species: Tetrahymena pigmentosa

C:Date: 15-Jul-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004

C:Accession: S50911

R:Piccinini, E.; Staudemann, W.; Albergoni, V.; de Gabrieli, R.; James, P.

Eur. J. Biochem. 226, 853-859, 1994

A:Title: Purification and primary structure of metallothioneins induced by cadmium in the presence of 1,10-phenanthroline

A:Reference number: S50911; MUID:95112850; PMID:7813475

A:Accession: S50911

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <PIC>

A:Cross-references: UNIPROT:P80394

C:Genetics:

A:Genetic code: SGC5

Query Match 9.1%; Score 94.5; DB 2; Length 104;

Best Local Similarity 34.3%; Pred. No. 1.8;

Matches 23; Conservative 8; Mismatches 29; Indels 7; Gaps 3;

QY 9 CDCAGDFHKKIGLFCR-----GCPAGHYLKAPCTEPCGNTCLVCPQDTFLAWHHNSE 64

Db 40 CTGTGEGCKTGCKCCQPAKSGCCGDKAKACCTDP--NSGC-CCSSKTNKCCDSTNKTE 96

QY 65 CARCOAC 71

Db 97 KTCCECC 103

RESULT 5

B21761

high cysteine chorion B 12 protein precursor - silkworm

C:Species: Bombyx mori (silkworm)

C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 11-Jan-2000

C:Accession: B21761

R:Iatrou, K.; Tsitilou, S.G.; Kafatos, F.C.

Proc. Natl. Acad. Sci. U.S.A. 81, 4452-4456, 1984

A:Title: DNA sequence transfer between two high-cysteine chorion gene families in the silkworm

A:Reference number: A21761; MUID:84272653; PMID:6589605

A:Accession: B21761

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-143 <IAT>

C:Superfamily: chorion class A protein pc292

Query Match 9.0%; Score 93.5; DB 2; Length 143;

Best Local Similarity 20.7%; Pred. No. 2.6;

Matches 36; Conservative 8; Mismatches 61; Indels 59; Gaps 8;

QY 9 CDCAGDFHKKIGLFCRGCPCAGHYLKAPCTEPCGNTCLVC-----PQDTFLAW 57

Db 24 CGC-----CCRGCGCG-----CGCGCGCCENFRVCSNSAAPTGLSICS 62

QY 58 ENHNSSECARCOACDEQASQVALENCSSAVADTRCGCKPGWFVECVQSVCSPPYQPC 117

Db 63 ENRYKGDVVC---VCGEVPFLGTADVCGNMCSSGCGCID-----YCGGNGCVGITRSC 111

QY 118 LDCGALHRRHRLLCRRDDTCGLPGFYEHGDCGVCPTSTLGCPCPCRCAAVC 171

Db 112 GCGCG-----GCGCG-----GCGCGCG-----GCCGCGSCGRSC 139

RESULT 6

146489

cysteine-rich hair keratin associated protein - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C:Accession: 146489; S49201



A:Reference number: A92978

A:Accession: B92978

A:Molecule type: protein

A:Residues: 1-131 <JOU>

A:Cross-references: UNIPROT:P02442

A:Experimental source: Angora breed

C:Comment: Wool and hair consist of microfibrils embedded in a rigid matrix of other proteins

C:Superfamily: keratin high-sulfur matrix protein IIIA

C:Keywords: duplication; hair

```
Query Match      8.0%; Score 83.5; DB 1; Length 131;
Best Local Similarity 22.8%; Pred. No. 13;
Matches 42; Conservative 5; Mismatches 46; Indels 91; Gaps 14;

QY  2  GGTRSPRC---DCAGDFHKKIGLFCRCGCPAGHYLKAP-----CT-----EPCGNSTCLV 48
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  16  GCGLPFCYRDPD-----CCRPVSCQTTVSRPTFVSRCTRFPCFRRPVC-- 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  49  CPQDTFLAWENHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFEVCQVSCQS 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  63  -----CDPCSLO-----EGC-----CRP-----ITCPTSC-- 83
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  109  SSPFYCQCLDGGALHRRLLCSRDDTCGLPGFVEHGDGVCVSCPTSLGSC-PERC 167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  84  -QAVVCRPC--CWA-----TTC--CQP-----VSQCPCCRPTSCQPAPC 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  168  AAVC 171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  119  RTTC 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 11

I47108

high-sulfur wool matrix protein B2C - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004

C:Accession: I47108

R:Rogers, G.R.; Hickford, J.G.; Bickerstaffe, R.

Anim. Genet. 25, 407-415, 1994

A:Title: Polymorphism in two genes for B2 high sulfur proteins of wool.

A:Reference number: I47105; MUID:95209146; PMID:7695121

A:Accession: I47108

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-152 <ROG>

A:Cross-references: UNIPROT:Q29620; GB:I33888; MID:g499874; PIDN:AA801447.1; PID:g940358

C:Superfamily: keratin high-sulfur matrix protein IIIA

```
Query Match      8.0%; Score 83.5; DB 2; Length 152;
Best Local Similarity 22.0%; Pred. No. 14;
Matches 39; Conservative 15; Mismatches 68; Indels 55; Gaps 10;

QY  23  CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCQACDEQASQVALEN 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  3  CCSTSFCCGFP1-CPTAGTCGSSCC-----RSTCSQTSCC--QPTSIQTS 44
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  83  CSAVADTRCGCKPGWFEVCQV-----SQCVSSSPFYCQP-----CL----- 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  45  CQPTCLQTSQCKTGCGIGSGYGVGSSGAVSSRTRWCRPDRCVGEVSLPPCCVSCGS 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  119  -DCGALHRRLLCSRDDTCG--TCLPGFVEHGDGVCVSCPTSLGSCPERCA-AVC 171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  105  PSSCQLYYAQASCC--RFSYCGQSCCR-----ACCCQPTCTEPVCEPTCSQPIC 152
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 12

I48298

cellular nucleic acid binding protein clone 14 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C:Accession: I48298; S1960

R:Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; T

Genomics 24, 14-19, 1994

A:Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identifier

A:Reference number: A55499; MUID:95203870; PMID:7896269

A:Accession: I48298

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-171 <RES>

A:Cross-references: UNIPROT:P53996; EMBL:Z11871; MID:g50474; PIDN:CAA77897.1; PID:g50475

C:Superfamily: cellular nucleic acid-binding protein

```
Query Match      8.0%; Score 83.5; DB 2; Length 171;
Best Local Similarity 26.8%; Pred. No. 15;
Matches 34; Conservative 13; Mismatches 59; Indels 21; Gaps 7;

QY  8  RDCAGDFHKKIGL---FCCRGCPAGHYLKAPCTEP-----CGNSTCLVCPQDTFLAWEN 58
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  49  RCGSGHLAKDCDLQEDACYNCGRGGHIAKDCKEKREREQC---CYNCGKPGHLARDC 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  59  NHHNSECARCAOCDEQASQVALENCSAVADTRCGCKPGWFEVCQVSCVSSSPFYCQPCLD 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  105  CDHADE-QKVCSCGEFGH--IQDCTKVKYRCG-ETGHV-----AINGSKTSEVNCYRCG 156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  119  DCGALHR 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  157  ESGHLAR 163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 13

A55499

zinc finger protein 9 - human

N:Alternate names: nucleic acid binding protein

C:Species: Homo sapiens (man)

C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 24-Sep-1999

C:Accession: A55499

R:Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; T

Genomics 24, 14-19, 1994

A:Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identifier

A:Reference number: A55499; MUID:95203870; PMID:7896269

A:Accession: A55499

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-170 <RES>

A:Cross-references: GB:L12693; MID:g292347; PIDN:AAA89198.1; PID:g292348

C:Genetics:

A:Gene: GDB:ZNF9

A:Cross-references: GDB:125342; OMIM:116955

A:Map position: 3q13.3-3q24

C:Superfamily: cellular nucleic acid-binding protein

```
Query Match      8.0%; Score 83; DB 2; Length 170;
Best Local Similarity 27.0%; Pred. No. 17;
Matches 34; Conservative 13; Mismatches 59; Indels 20; Gaps 7;

QY  8  RDCAGDFHKKIGL---FCCRGCPAGHYLKAPCTEP-----CGNSTCLVCPQDTFLAWEN 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  49  RCGSGHLAKDCDLQEDACYNCGRGGHIAKDCKEKREREQC---CYNCGKPGHLARDC 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  60  HHHNSECARCAOCDEQASQVALENCSAVADTRCGCKPGWFEVCQVSCVSSSPFYCQPCLD 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  105  DHADE-QKVCSCGEFGH--IQDCTKVKYRCG-ETGHV-----AINGSKTSEVNCYRCGE 156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  120  CGALHR 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  157  SGHLAR 162
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 14

I48297

cellular nucleic acid binding protein clone 6 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C:Accession: I48297; S19861; S19959

R:Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; T

Genomics 24, 14-19, 1994

Search completed: June 27, 2005, 14:19:24  
Job time : 40 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2005, 14:05:01 ; Search time 173 Seconds  
(without alignments)  
515.039 Million cell updates/sec

Title: US-10-081-280-6\_COPY\_25\_198

Perfect score: 1038

Sequence: 1 QGTRSPRCAGDFHKKIG.....CPTSTLGCSPERCAAVCGWR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 561438

Minimum DB seq length: 0

Maximum DB seq length: 174

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	165.5	15.9	150	2 Q9R230	Q9R230 rattus norv
2	161.5	15.6	130	2 Q8MJ20	Q8MJ20 macaca mula
3	146.5	14.1	146	2 Q7Z2Y4	Q7Z2Y4 gallus gall
4	135	13.0	147	2 Q8SQ52	Q8SQ52 felis silve
5	133.5	12.9	124	2 Q8SQ51	Q8SQ51 felis silve
6	127.5	12.3	169	2 Q8JKE0	Q8JKE0 rattus norv
7	126.5	12.2	65	2 Q8SQ49	Q8SQ49 felis silve
8	125	12.0	110	2 Q9BIR2	Q9BIR2 paramacium
9	124	11.9	110	2 Q9BIR3	Q9BIR3 paramacium
10	124	11.9	117	2 Q6VZRI	Q6VZRI canarypox v
11	123	11.8	167	2 Q8BDC5	Q8BDC5 human cytom
12	121.5	11.7	172	2 Q91IR0	Q91IR0 human cytom
13	119	11.5	151	2 Q8F2H9	Q8F2H9 homo sapien
14	111.5	10.7	166	2 Q8BDC6	Q8BDC6 human cytom
15	109	10.5	118	2 Q8WTI6	Q8WTI6 thresophila
16	108.5	10.5	171	2 Q7TFH9	Q7TFH9 thresus cyto
17	106.5	10.3	174	2 Q8N2N0	Q8N2N0 bombyx mori
18	105	10.1	137	2 Q61TV8	Q61TV8 branchiosto
19	104.5	10.1	167	2 Q9DJL2	Q9DJL2 cowpox viru
20	104	10.0	169	1 KRUA HUMAN	P26371 homo sapien
21	103.5	10.0	167	2 Q72F62	Q72F62 cowpox viru
22	103.5	10.0	167	2 Q8UYL3	Q8UYL3 vaccinia vi
23	103	9.9	169	2 Q14564	Q14564 homo sapien
24	102.5	9.9	167	2 Q8BDC3	Q8BDC3 human cytom
25	100.5	9.7	166	2 Q8BDC4	Q8BDC4 human cytom
26	100	9.6	90	2 Q6SC66	Q6SC66 camelpox vi
27	98.5	9.5	167	2 Q8BDC7	Q8BDC7 human cytom
28	98	9.4	170	2 Q9D548	Q9D548 mus musculus
29	97.5	9.4	167	2 Q701N3	Q701N3 homo sapien
30	97	9.3	142	2 Q919J2	Q919J2 xenopus lae
31	97	9.3	148	2 Q57093	Q57093 cowpox viru

32 97 9.3 173 2 Q6ISF6 Q6ISF6 homo sapien  
33 96.5 9.3 168 2 Q9D732 Q9D732 mus musculus  
34 96 9.2 174 1 KR92 HUMAN KR92 homo sapien  
35 94.5 9.1 107 1 MT1\_TETPI MT1\_TETPI  
36 94.5 9.1 107 1 MT1\_TETTH MT1\_TETTH  
37 94 9.1 143 2 Q91J33 Q91J33 xenopus lae  
38 93.5 9.0 107 1 MT1\_TETPY MT1\_TETPY  
39 92.5 8.9 160 2 Q83022 Q83022 thresophila  
40 92.5 8.9 160 2 Q9RAD6 Q9RAD6 rhodobacter  
41 92 8.9 155 2 Q6Y1L9 Q6Y1L9 thresophila  
42 92 8.9 165 2 Q6L8G8 Q6L8G8 homo sapien  
43 91.5 8.8 129 2 Q6L8G9 Q6L8G9 homo sapien  
44 91.5 8.8 136 1 KR42\_HUMAN KR42\_HUMAN  
45 91.5 8.8 139 2 Q8RYZ5 Q8RYZ5 oryza sativ

#### ALIGNMENTS

RESULT 1  
Q9R230 PRELIMINARY; PRT; 150 AA.  
ID Q9R230  
AC Q9R230;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Fas receptor (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX MBL; TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Wistar; TISSUE=Corpus luteum;  
RA Lareu R.R., Dharmarajan A.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF104034; AAD20221.1; -;  
DR HSSP; Q92956; IJMA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:0007185; P:signal transduction; IEA.  
DR InterPro; IPR008063; Fas\_receptor.  
DR Pfam; PF00020; TNFR\_c6.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00208; TNFR\_2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
KW NON TER  
FT NON TER 150 150  
SQ SEQUENCE 150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;

Query Match 15.9%; Score 165.5; DB 2; Length 150;

Best Local Similarity 30.8%; Pred. No. 1.7e-06;

Matches 32; Conservative 13; Mismatches 52; Indels 7; Gaps 2;

Qy 18 KIGLFCRCGCPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNHSECARCQACDEQASQ 77  
Db 45 QVGFPCQCPQPGERKVKDCTSGAPTCHPCTGEEYTDKHYSDKRCRCACFDEGHGL 104  
Qy 78 VALENCASAVADTRCGCKPGFVEQVSCVSSSPFYCQPCLDGC 121  
Db 105 EVEINCTRTQTKCRKENFY--CNASLC-----DHCYHCTSCG 141

#### RESULT 2

Q8MJ20 PRELIMINARY; PRT; 130 AA.  
ID Q8MJ20  
AC Q8MJ20;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fas receptor CD95 (Fragment).
OS Macaca mulatta (rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnoult D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
RA Estaquier J.
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530075; AAM95635.1; -.
DR HSSP; O14763; 1DU3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR Pfam; PF0020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON_TER 1
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 14814 MW; 91542C61323F3C27 CRC64;

Query Match 15.6%; Score 161.5; DB 2; Length 130;
Best Local Similarity 31.7%; Pred. No. 3.3e-06;
Matches 32; Conservative 12; Mismatches 50; Indels 7; Gaps 1;

QY 20 GLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNSECARCOAQDEQASQVA 79
Db 22 GQCRNCPGPKERKARDCTVNEBDFPCVCGEGKEYTDGKHFSSKRCRLCDGEGHLEV 81

QY 80 LENCASAVADTRCGCKPGWFVBCQVSSSPPFYCQPCLDLC 120
Db 82 EINCTRTQNTKCRCKPNFF-----CNSAVCEHCDPCTKC 115

RESULT 3
ID Q7ZZY4 PRELIMINARY; PRT; 146 AA.
AC Q7ZZY4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Osteoprotegerin (Fragment).
GN Name=OPG;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22760275; PubMed=12878204; DOI=10.1016/S0006-291X(03)01304-4;
RA Bridgman J.T., Johnson A.L.;
RT "Characterization of chicken TNFR superfamily decoy receptors, Dcr3
and osteoprotegerin."
RL Biochem. Biophys. Res. Commun. 307:956-961(2003).
DR EMBL; AY251407; AAP03890.1; -.
DR HSSP; O14763; 1DAV.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGFLike.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
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DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16487 MW; 1C9B64FE3A0FC2DF CRC64;

Query Match 14.1%; Score 146.5; DB 2; Length 146;
Best Local Similarity 28.3%; Pred. No. 6.6e-05;
Matches 39; Conservative 13; Mismatches 49; Indels 37; Gaps 7;

QY 24 CRGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNSECARCOA-CDEQASQVALEN 82
Db 41 CNQCPGSGYVQKCT-AASTVTCAPCP-DQYAAEDWNSNDECCQVCSAVCKE--LQYIKQE 96

QY 83 CSAVADTRCGCKPGWFVBCQVSSSPPFYCQPCLDGALHRRHRLLCRRDTC----- 138
Db 97 CTSTQDRVCCEIGWYLELF-----CL-----KHTECPPGF 128

QY 139 GTCLPGFYEHGDCVSCP 156
Db 129 GVAQGPPESDTVCFCCP 146

RESULT 4
ID Q8SQ52 PRELIMINARY; PRT; 147 AA.
AC Q8SQ52;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fas (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
RT "Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
cells."
RL Eur. J. Immunogenet. 31:159-166(2004).
DR EMBL; AB072009; BAB86798.1; -.
DR HSSP; O14763; 1DAV.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT NON_TER 1
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16751 MW; 0E192AC4DCE1001F CRC64;

Query Match 13.0%; Score 135; DB 2; Length 147;
Best Local Similarity 27.4%; Pred. No. 0.00062;
Matches 32; Conservative 15; Mismatches 32; Indels 38; Gaps 6;

QY 59 NHNHNSECARCOA-CDEQASQVALENCSAVADTRCGCKPGWFVBCQVSSSPPFYCQPC 118
Db 10 SHFSPRCRCKICDEEHGLEVEKNCTRTQNTKCRCKSNFF--CNVSQC-----DHCNFCM 62

QY 119 DCGALHRRHRLLCRRDTCGTCPLPGFYEHG--DGCVSCPTSTLGCSPERCAAVCGW 173
Db 63 MC-----EHGILENCT--PTSNY-KCKQSSSSKLLW 90
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[illegible]



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FT   NON TER      1
SQ   SEQUENCE     65 AA; 7670 MW;  A557395A3D527417 CRC64;

Query Match              12.2%; Score 126.5; DB 2; Length 65;
Best Local Similarity    36.7%; Pred. No. 0.0016;
Matches                  22; Conservative 11; Mismatches 20; Indels 7; Gaps 2;

Qy  59 NHHNSECARCOACDEQAQSVALENCASAVADTRCGCKEFGWFVECVSCVSSSPFYCQPCL 118
    :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db  10 SHFSPCRKRCKICDEEHGLEVKENCTRTONTKRCRKSNNF--CNVSQC-----DHCHNPM 62

RESULT 8
Q9BIR2 PRELIMINARY; PRT; 110 AA.
AC Q9BIR2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Furin-like protein (Fragment).
GN Name=fur;
OS Paramesicium aurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramesicium.
OX NCBI_TaxID=5889;
RN [1]
RC STRAIN=2998-axenic;
RA Wyroba E., Wiejak J., Surmacz L.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF351195; AAK27160.1; -.
DR InterPro; IPR006209; EGF like.
DR Prosite; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
FT   NON TER      1
SQ   SEQUENCE     110 AA; 11810 MW;  449EOD07D8BB0A91 CRC64;

Query Match              12.0%; Score 125; DB 2; Length 110;
Best Local Similarity    22.4%; Pred. No. 0.0034;
Matches                   35; Conservative 17; Mismatches 52; Indels 52; Gaps 7;

Qy  8 RDCAGDFHKKIGLFCCRGCPAGHYLKAPCTPCGNSITCLVCPODTFLAWNHHSSEAR 67
    :|:::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db  5 KCICSSNYYSLSLVLRAC-----ISPCLCLELDDA--LALPAD-----GTQCVT 47

Qy  68 QCACDEQAQSVALENCASAVADTRCGCKEFGWFVECVSCVSSSPFYCQPCLDGALHRHT 127
    :|:::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db  48 CQP-----GLNRIIDNVNKNCILGDYETTTGVLAQTCSF----PCYDC----- 88

Qy  128 RLCCSRRDTCGTCLPGFYEHGGDCVSCPSTLGSC 163
    :|:::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db  89 -----ADNGT-----GAECTTCPPTTLFC 108

RESULT 9
Q9BIR3 PRELIMINARY; PRT; 110 AA.
AC Q9BIR3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Furin-like protein (Fragment).
GN Name=fur;
OS Paramesicium aurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramesicium.
OX NCBI_TaxID=5889;
RN [1]
RC STRAIN=2998-axenic;
RA Wyroba E., Wiejak J., Surmacz L.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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[illegible]

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Db 92 QOKGTSETDTICTCEGW-----HCTSEA---CESCV---LHR-----123
Qy 140 TCLPGF 145
Db 124 SCSPGF 129

RESULT 14
Q8BDC6 ID Q8BDC6 PRELIMINARY; PRT; 166 AA.
AC Q8BDC6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE UL144 (Fragment).
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A. PubMed=12355354;
RX MEDLINE=22424165; Willoughby R.E., Pass R.F., Zong J.C., Jang W.J.,
RA Arav-Boger R., Hayward G.S.;
RA "Polymorphisms of the cytomegalovirus (CMV)-encoded tumor necrosis
RT factor-alpha and beta-chemokine receptors in congenital CMV disease.";
RL J. Infect. Dis. 186:1057-1064(2002).
DR EMBL; AF498087; AAN37946.1; -.
DR HSSP; Q92956; 1JNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR.c6.
DR Pfam; PF00020; TNFR.c6; 1.
DR SMART; SM00208; TNFR; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
FT NON TER 166
SQ SEQUENCE 166 AA; 18411 MW; 193D55AE19E046FA CRC64;

Query Match 10.7%; Score 111.5; DB 2; Length 166;
Best Local Similarity 28.6%; Pred. No. 0.066;
Matches 22; Conservative 20; Mismatches 28; Indels 7; Gaps 4;

Qy 18 KIGLFCRCGCPAGHYLKAPCTPCGNSLTCVCPQDTFLAWNHNSCARCQACQEQASQ 77
Db 29 QLGNCQCPCKQGYRVTCQCTQ-YTSTICTLCPNGTVYS--GLYN--CTNCTECND--TE 81
Qy 78 VALENCSAVADTRCGCK 94
Db 82 VTRNCTSTNNVTCASK 98

RESULT 15
Q8WTI6 ID Q8WTI6 PRELIMINARY; PRT; 118 AA.
AC Q8WTI6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE PFAIRE-interacting factor 2 (CG31483-PA).
GN Name=pfif2; Synonyms=PIF-2; ORFNames=CG31483;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22667250; PubMed=12782278; DOI=10.1016/S0925-4773(03)00019-4;
RA Rascle A., Stowers R.S., Garza D., Lepesant J.-A., Hogness D.S.;
RA "L63, the Drosophila PFAIRE, interacts with two novel proteins
RT unrelated to cyclins.";
RL Mech. Dev. 120:617-628(2003).
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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush K., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodagef, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RL melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RL a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
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RT systematic review.";
RN Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF273708: AAL35411.1; -
DR EMBL: AE003674: AAF54113.3; -
DR HSP: P21860: IMGB.
DR FlyBase: FEGn0046873; Pif2.
DR PROSITE: PS01208; VMFC_1; UNKNOWN_1.
SQ SEQUENCE 118 AA; 11566 MW; AF6FD15A61FF5C81 CRC64;

Query Match      10.5%; Score 109; DB 2; Length 118;
Best Local Similarity 23.8%; Pred. No. 0.08;
Matches 41; Conservative 3; Mismatches 62; Indels 66; Gaps 10;

Qy      6  S P R C - D C A G D F H K K I G L F C C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T F L A W E N H H N S E 64
Db      3  S P C G S C C G P - - - - - C C S P C - - - - - C S P C C P P C C N D C G S C - - - - - 33

Qy     65  C A R C Q A C D E Q A S Q V A L E N C S A V A D T R C G - - C K P G W F V E C Q V S Q C V S S P F Y C Q P C L D C G A 122
Db     34  - - - C S P C - - - - - C G P C C S P C G P C C S P - - - - - C C S P C C T P C C T P C C T P C C K C - - 72

Qy    123  L H R H T R L L C S R R D T D C G T - - C L P G F Y E H G D G C V S C P T S T L G S C P E R C A A V C G 172
Db     73  - - - - - C T P C C V P C C T P C C T P C C T P - - - - - C C T P C C S P C C G P C C S P C G 113
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Search completed: June 27, 2005, 14:22:24  
Job time : 175 secs

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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:03:05 ; Search time 162 Seconds  
(without alignments)  
415.409 Million cell updates/sec

Title: US-10-081-280-6\_COPY\_25\_198

Perfect score: 1038

Sequence: 1 QGTRSPRCAGDFHKKIG.....CPTSTLSCSPERCAAVCGWR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1382563

Minimum DB seq length: 0  
Maximum DB seq length: 174

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206.5	19.9	161	6	ABR62365 Tumour ne
2	200.5	19.3	154	6	AAY94711 Tumour ne
3	200.5	19.3	154	6	ADA49698 Extracell
4	200.5	19.3	154	7	ADL17741 Human tum
5	200.5	19.3	154	8	ADJ56814 Human TNF
6	200.5	19.3	161	2	ABG74752 Human TNF
7	200.5	19.3	161	2	AAR27496 Native 30
8	200.5	19.3	161	2	AAW59664 Human sol
9	200.5	19.3	161	2	AAW52267 Soluble t
10	200.5	19.3	161	2	AAW89233 Tumour ne
11	200.5	19.3	161	4	AB37676 Human 30
12	200.5	19.3	161	6	ABR62363 Tumour ne
13	200.5	19.3	161	6	ADA20577 Human 30k
14	200.5	19.3	161	6	ADA20579 Human 30k
15	200.5	19.3	161	8	ADH78698 Human tum
16	198.5	19.1	162	5	AAM48058 Human TNF
17	197.5	19.0	161	6	ABR62364 Tumour ne
18	197	19.0	32	4	AB84943 Human TR3
19	196	18.9	139	4	AB66977 Peptide: wild type
20	196	18.9	139	5	ABG71825 Wild type
21	196	18.9	139	8	ADM28814 Human TNF
22	190	18.3	32	8	ADH50950 Altered T
23	182	17.5	148	6	ABU60689 Human mat
24	182	17.5	155	6	ABU60676 Human mat
25	182	17.5	159	6	ABU60683 Human mat

26	181.5	17.5	161	7	ADL17744	Adl17744 Human TRA
27	181.5	17.5	161	8	ADJ56817	Adj56817 Human TR2
28	170.5	16.4	159	2	AAR24083	Aar24083 Truncated
29	165.5	15.9	169	2	AAR78612	Aar78612 Plasmid f
30	165.5	15.9	170	3	AAB36228	Aab36228 Rat Fas r
31	165	15.9	125	4	AAB37675	Aab37675 Human 30
32	164.5	15.8	148	8	ADM46624	Adm46624 Mouse 7F4
33	162.5	15.7	119	6	ADA49701	Ada49701 Extracell
34	162.5	15.7	144	2	AAW50286	Aaw50286 Human Fas
35	162.5	15.7	159	2	AAW50288	Aaw50288 Human Fas
36	162.5	15.7	167	6	ADA49708	Ada49708 Extracell
37	162.5	15.7	173	3	AAB36229	Aab36229 Human Fas
38	161	15.5	168	2	AAR24084	Aar24084 Truncated
39	155.5	15.0	133	7	ABW02714	Abw02714 Mouse tms
40	155.5	15.0	133	8	ADJ45750	Adj45750 Murine tm
41	152.5	14.7	158	2	AAR24081	Aar24081 Truncated
42	149.5	14.4	110	2	AAW52268	Aaw52268 Truncated
43	147.5	14.2	117	8	ADF57549	Adf57549 Mouse ymk
44	147	14.2	101	2	AAW52276	Aaw52276 Truncated
45	147	14.2	101	2	AAW89238	Aaw89238 Protein S

ALIGNMENTS

RESULT 1  
ABR62365  
ID ABR62365 standard; protein, 161 AA.  
XX ABR62365;  
AC  
XX 22-SEP-2003 (first entry)  
DT  
XX  
DE Tumour necrosis factor receptor extracellular domain H23P mutant.  
XX  
KW Tumour necrosis factor; receptor; TNFRp; proline; protein engineering;  
KW mutant; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 23 /note= "wild-type His substituted by Pro"  
FT Misc-difference 46 /note= "wild-type Ser substituted by Ile"  
FT  
XX  
PN WO2003046160-A2.  
XX  
PD 05-JUN-2003.  
XX  
PF 21-NOV-2002; 2002WO-EP013059.  
XX  
PR 30-NOV-2001; 2001US-0340648P.  
XX  
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
XX  
PI Brondyk W, Jiang X, Schweickhardt RL;  
XX  
DR WPI; 2003-523245/49.  
XX  
CC Increasing expression of a protein, comprises substituting at least one codon in the polynucleotide encoding the protein, for a codon encoding proline.  
XX  
PS Example 2; Page; 53pp; English.  
XX  
CC This is the protein sequence of a mutated extracellular domain of the p55 tumour necrosis factor receptor (TNFRp) in which a Pro residue  
CC substitutes the native His-34 residue (residue 23 in the present  
CC sequence) and an Ile residue substitutes the native Ser-57 residue  
CC (residue 46 of the present sequence). Screening of TNFRp mutant clones  
CC using a yeast display system yielded a clone that showed a higher

expression level in yeast than did a wild-type TNFR1 clone. The encoded polypeptide contained these 2 amino acid substitutions. The introduction of proline residues may assist the polypeptide to adopt a favourable conformation that fixes the neighbouring cysteine residue into the correct orientation for disulfide bond formation, resulting in a higher yield of correctly folded proteins in yeast or mammalian host cells. The invention therefore provides methods of increasing protein expression levels by substituting an amino acid residue with proline, where the substitution occurs within 15 (preferably within 10, and especially within 5) amino acids of a cysteine residue. Note: the present sequence is not shown in the specification but is derived from the TNFR1 sequence given in figure 4 (see ABR62363)

XX Sequence 161 AA;

Query Match 19.9%; Score 206.5; DB 6; Length 161;

Best Local Similarity 30.4%; Pred. No. 6.2e-08;

Matches 49; Conservative 20; Mismatches 71; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQOA 75

Db 11 HPQNNISICTCKPKGTLYNDPCPGQDTCRECEISFTASENHLR-HCLSCSKCRKEM 69

Qy 76 SQVALENCASAVADTRCCCKPGWFVEEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCS 132

Db 70 GQVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCLN-GTVH----LSCQ 119

Qy 133 RRDTDCGTCPLPGFVEHGDGCVSCPTSTLGSCE--RCAAVC 171

Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 155

RESULT 2

AAY94711

ID AAY94711 standard; protein; 154 AA.

XX AC AAY94711;

XX DT 29-JAN-2001 (first entry)

XX DE Tumour necrosis factor receptor (TNFR) domain of TNFR-1.

XX KW Tumour necrosis factor-receptor related protein; TR2; human; cancer; chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease; immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID; severely combined immunodeficiency; apoptosis inhibition; Alzheimer's disease; Parkinson's disease; Crohn's disease.

XX OS Homo sapiens.

XX PN WO200056405-A2.

XX PD 28-SEP-2000.

XX PF 22-MAR-2000; 2000WO-US007521.

XX PR 22-MAR-1999; 99US-0125683P.

XX PR 26-MAR-1999; 99US-0126522P.

XX PR 20-MAY-1999; 99US-0135169P.

XX PR 06-AUG-1999; 99US-0147383P.

XX PA (NIJJ/) NI J.

XX PA (ROSE/) ROSEN C A.

XX PA (GENTZ/) GENTZ R L.

XX FI Ni J, Rosen CA, Gentz RL;

XX DR WPI; 2000-594519/56.

XX PT Nucleic acid molecule encoding a human tumor necrosis factor receptor 2 and its two splice variants, useful for treating arthritis or inflammation, cancer (such as follicular lymphomas) and immunodeficiency disorders.

XX PS Disclosure; Fig 16; 373pp; English.

XX CC This invention relates to an isolated nucleic acid molecule encoding a human tumor necrosis factor (TNF)-receptor related protein TR2. Included in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2. The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a member of the TNFR superfamily. The invention includes a method for the treatment of arthritis or inflammation using an antibody directed against a fragment of the TR2 protein. TR2 its agonists, antagonists and antibodies exhibit cytostatic, dermatological, antianemic, immunosuppressive, anti-allergic, antiarthritic, antiasthmatic, anti-inflammatory, neuroprotective, nootropic, antiparkinsonian, and cerebroprotective activity. The methods are useful for treating arthritis or inflammation, cancer (such as follicular lymphomas, carcinoma with p53 mutations, cardiac tumors, pancreatic, breast, or prostate cancer), an immunodeficiency or for enhancing an in vivo leukocyte response to an antigen. Anti-TR2 antibodies are useful for treating, inhibiting or preventing autoimmune diseases (such as autoimmune hemolytic anaemia, dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and inflammatory myopathies) and immunodeficiency disorders (such as severely combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2, TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or antagonists are useful for treating or preventing autoimmune diseases and inhibit the growth, progression and/or metastasis of cancers. They are also used to activate, differentiate or proliferate cancerous cells or tissues, and can be used to treat diseases associated with increased cell survival, or the inhibition of apoptosis, e.g. Alzheimer's disease, Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful as sources for generating antibodies, as molecular weight markers. This sequence represents the tumor necrosis factor receptor (TNFR) domain of the human TNFR-1 protein. The sequence was used in the characterisation of the TR2 receptor protein of the invention

XX SQ Sequence 154 AA;

Query Match 19.3%; Score 200.5; DB 3; Length 154;

Best Local Similarity 29.8%; Pred. No. 1.7e-07;

Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQOA 75

Db 9 HPQNNISICTCKPKGTLYNDPCPGQDTCRECEISFTASENHLR-HCLSCSKCRKEM 67

Qy 76 SQVALENCASAVADTRCCCKPGWFVEEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCS 132

Db 68 GQVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCLN-GTVH----LSCQ 117

Qy 133 RRDTDCGTCPLPGFVEHGDGCVSCPTSTLGSCE--RCAAVC 171

Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 153

RESULT 3

ADA49698

ID ADA49698 standard; protein; 154 AA.

XX AC ADA49698;

XX DT 20-NOV-2003 (first entry)

XX DE Extracellular region of human TNFR1 (htNFR1) protein.

XX KW Apo-2 ligand inhibitor; Apo-2L; Apo-3; apoptosis; affinity; competitive-type receptor; binding assay; cancer cell; human; TNF receptor family; htNFR1; cytostatic.

XX OS Homo sapiens.

XX PN US2002192729-A1.

XX PD 19-DEC-2002.

XX PF 28-MAR-2002; 2002US-00112793.  
XX PR 01-APR-1996; 96US-00625328.  
XX PR 23-SEP-1996; 96US-00710802.  
XX PR 31-MAR-1997; 97US-00828683.  
XX PA (GETH ) GENENTECH INC.  
XX PI Ashkenazi AJ;  
XX PI WPI; 2003-657226/62.  
XX DR Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or  
XX PT Apo-3 polypeptide which induces or stimulates apoptotic activity, useful  
XX PT in diagnostic assays.  
XX PS Disclosure; Fig 2; 53pp; English.  
XX CC The present invention relates to the isolation of a biologically active  
XX CC Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide  
XX CC sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The  
XX CC Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI  
XX CC is useful for generating antibodies, as standards in assays for Apo-3 or  
XX CC Apo-2LI, in affinity purification techniques, and in competitive-type  
XX CC receptor binding assays when labelled with radioiodine, enzymes or  
XX CC fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or  
XX CC inducing apoptosis in cancer cells, and thus have therapeutic utility.  
XX CC The present sequence represents the extracellular region of a human TNF  
XX CC receptor family protein. This sequence is compared with the extracellular  
XX CC region of human Apo-2LI.  
XX SQ Sequence 154 AA;  
Query Match 19.3%; Score 200.5; DB 6; Length 154;  
Best Local Similarity 29.8%; Pred. No. 1.7e-07;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
QY 16 HKKIGLCRCGCPAGHYLKAPCTPCGNSSTCLVCPQDTFLAWENHNHSECARCOACDQA 75  
Db 9 HPQNNISICTKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 67  
QY 76 SQVALENCASVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDCLCGALHRRHRLCLS 132  
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQC-----FNCSLCIN-GTVH----LSCQ 117  
QY 133 RRDTDCGTCGFGYEHGDCVCSTSLGSCPE--RCAAVC 171  
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 153  
RESULT 4  
ID ADL17741 standard; protein; 154 AA.  
AC ADL17741;  
XX 06-MAY-2004 (first entry)  
DE Human tumour necrosis factor receptor-I cysteine rich motif.  
XX Human; apoptosis inducing molecule II; AIM II; antibody;  
KW tumour necrosis ligand superfamily; lymphotoxin-beta receptor; TR6;  
KW TRAIL receptor 6; lymphadenopathy; aberrant bone development;  
KW autoimmune disease; graft-versus-host disease; rheumatoid arthritis;  
KW osteoarthritis; cancer; apoptosis.  
OS Homo sapiens.  
XX US6635743-B1.  
PN 21-OCT-2003.  
XX 21-OCT-2003.  
XX

PF 10-MAR-2000; 2000US-00523323.  
XX PR 22-MAR-1996; 96US-0013923P.  
XX PR 31-OCT-1996; 96US-0030157P.  
XX PR 21-MAR-1997; 97US-00822953.  
XX PR 07-JAN-1998; 98US-00003886.  
XX PR 20-FEB-1998; 98US-00027287.  
XX PR 20-FEB-1998; 98US-0075409P.  
XX PR 19-FEB-1999; 99US-00252656.  
XX PR 11-MAR-1999; 99US-0124041P.  
XX PR 04-JUN-1999; 99US-0137457P.  
XX PR 06-JUL-1999; 99US-0142657P.  
XX PR 11-AUG-1999; 99US-0148326P.  
XX PR 02-DEC-1999; 99US-0168380P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Ebner R, Yu G, Ruben SM, Ullrich S, Zhai Y;  
XX WPI; 2003-810570/76.  
XX DR New antibody that binds to human Apoptosis Inducing Molecule II (AIM II)  
XX PT protein, useful for preparing a composition for treating e.g.,  
XX PT lymphadenopathy, autoimmune disease, rheumatoid arthritis, osteoarthritis  
XX PT or cancer.  
XX Example 13; SEQ ID NO 53; 163pp; English.  
XX The invention relates to an isolated antibody or its portion binding to a  
XX protein comprising a protein whose sequence comprises an immunogenic  
XX fragment of the amino acid residues 68-240 of the Human Apoptosis  
XX inducing molecule II, AIM II, appearing as ADL17690 or a protein whose  
XX sequence comprises a fragment of amino acid residues 68-240, where the  
XX fragment comprises at least 30 or 50 amino acid residues. Also included  
XX are a hybridoma that produces the antibody, a method of detecting in a  
XX biological sample a protein that binds the antibody or its portion, a  
XX composition comprising the antibody and a carrier and an isolated cell  
XX that produces the antibody. Human AIM II is a member of the tumour  
XX necrosis ligand superfamily and has been shown to bind lymphotoxin-beta  
XX receptor and TR6 (TRAIL receptor 6). The antibody is useful for preparing  
XX a composition for treating e.g., lymphadenopathy, aberrant bone  
XX development, autoimmune disease, graft-versus-host disease, rheumatoid  
XX arthritis, osteoarthritis or cancer (many other diseases and conditions  
XX are listed in the specification). The present sequence represents a  
XX cysteine-rich motif from a protein thought to bind AIM II.  
XX SQ Sequence 154 AA;  
Query Match 19.3%; Score 200.5; DB 7; Length 154;  
Best Local Similarity 29.8%; Pred. No. 1.7e-07;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
QY 16 HKKIGLCRCGCPAGHYLKAPCTPCGNSSTCLVCPQDTFLAWENHNHSECARCOACDQA 75  
Db 9 HPQNNISICTKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 67  
QY 76 SQVALENCASVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDCLCGALHRRHRLCLS 132  
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQC-----FNCSLCIN-GTVH----LSCQ 117  
QY 133 RRDTDCGTCGFGYEHGDCVCSTSLGSCPE--RCAAVC 171  
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 153  
RESULT 5  
ADJ56814  
ID ADJ56814 standard; protein; 154 AA.  
XX AC ADJ56814;  
XX 06-MAY-2004 (first entry)  
XX





DT 25-MAR-2003 (revised)  
XX 09-MAR-1993 (first entry)  
XX  
DE Native 30 kD TNF inhibitor.  
XX  
KW Tumour necrosis factor; ethylene glycol; pharmacokinetic;  
KW adult respiratory distress syndrome; rheumatoid arthritis; septic shock;  
KW pulmonary fibrosis; spacer.  
XX  
OS Homo sapiens.  
XX  
XX WO9216221-A1.  
XX  
XX 01-OCT-1992.  
XX  
XX 13-MAR-1992; 92WO-US002122.  
XX  
XX 15-MAR-1991; 91US-00669862.  
XX  
XX 17-JAN-1992; 92US-00822236.  
XX  
XX (SYND ) SYNERGEN INC.  
XX  
XX Thompson RC, Armes LG, Evans RJ, Brewer MT, Kohno T;  
XX  
XX WPI; 1992-348933/42.  
XX  
XX New ethylene! glycolated polypeptide(s) with improved pharmacokinetic  
XX properties - for treating e.g. TNF and IL-1 mediated diseases, e.g. adult  
XX respiratory distress syndrome, rheumatoid arthritis, septic shock etc.  
XX  
XX Claim 54; Fig 2; 100pp; English.  
XX  
XX The sequence shows a native 30 kD TNF inhibitor which may be modified to  
XX contain at least one non-native cysteine residue, pref. at positions 1,  
XX 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-  
XX peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such  
XX TNF inhibitor mols. may be linked via this non-peptidic spacer. The  
XX modified polypeptides show improved pharmacokinetic properties, i.e.  
XX increased mol. wt. hence reduced clearance rate following s.c. or  
XX systemic administration, increased sol. of native TNF inhibitors, and  
XX reduced antigenicity. The polypeptides may be used for treatment of TNF  
XX mediated diseases such as adult respiratory distress syndrome, pulmonary  
XX fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic  
XX shock. The same method may be applied to the interleukin-1 receptor  
XX antagonist IL-1ra. See also AAR27495. (Updated on 25-MAR-2003 to correct  
XX PN field.)  
XX  
SQ Sequence 161 AA;  
  
Query Match 19.3%; Score 200.5; DB 2; Length 161;  
Best Local Similarity 29.8%; Pred. No. 1.8e-07;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
  
Qy 16 HKITGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75  
Db 11 HPQNNISICTKCHKGTLYNDCPGQDTCRECSGFTASENHLR-HCLSCSKCKEM 69  
  
Qy 76 SQVALENCASAVADTRCGCKPGWFVEEC---QVSQVSSSPFYCQPCDGCALHRRHRLCS 132  
Db 70 QGVEISSCTVDRDTCGCKKNQYRHYWSENLFQC-----FNCSLCLN-GTVH---LSCQ 119  
  
Qy 133 RRDTDCGTCPLGPFYEHGDCVCSTLGSQPE--RCAAVC 171  
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 155  
  
RESULT 8  
AAW59664  
ID AAW59664 standard; protein; 161 AA.  
XX  
AC AAW59664;  
XX  
DT 28-SEP-1998 (first entry)

XX Human soluble tumour necrosis factor receptor type I.  
XX  
XX Human; tumour necrosis factor; TNF; TNF receptor type I;  
KW inflammatory disease; leukaemia; TNF binding protein;  
KW anti-inflammatory drug; methotrexates.  
XX  
OS Homo sapiens.  
XX  
XX WO9824463-A2.  
XX  
XX 11-JUN-1998.  
XX  
XX 08-DEC-1997; 97WO-US022733.  
XX  
XX 06-DEC-1996; 96US-0032587P.  
XX  
XX 23-JAN-1997; 97US-0036355P.  
XX  
XX 07-FEB-1997; 97US-0039315P.  
XX  
XX 09-JUL-1997; 97US-0052023P.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Bendele AM, Sennello RM, Edwards CK;  
XX  
XX WPI; 1998-333039/29.  
XX  
XX N-ESDB; AAV41548.  
XX  
XX Treatment of acute or chronic inflammatory disease, e.g. leukaemia - by  
XX administering tumour necrosis factor binding protein and at least one  
XX additional anti-inflammatory drug, e.g. methotrexate.  
XX  
XX Disclosure; Fig 1; 104pp; English.  
XX  
XX This is the amino acid sequence of the human tumour necrosis factor  
XX receptor type I, used in the method of the invention involving the  
XX treatment of acute or chronic inflammatory disease such as leukaemia by  
XX administering tumour necrosis factor binding protein and at least one  
XX additional anti-inflammatory drug, e.g. methotrexate  
XX  
SQ Sequence 161 AA;  
  
Query Match 19.3%; Score 200.5; DB 2; Length 161;  
Best Local Similarity 29.8%; Pred. No. 1.8e-07;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
  
Qy 16 HKITGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75  
Db 11 HPQNNISICTKCHKGTLYNDCPGQDTCRECSGFTASENHLR-HCLSCSKCKEM 69  
  
Qy 76 SQVALENCASAVADTRCGCKPGWFVEEC---QVSQVSSSPFYCQPCDGCALHRRHRLCS 132  
Db 70 QGVEISSCTVDRDTCGCKKNQYRHYWSENLFQC-----FNCSLCLN-GTVH---LSCQ 119  
  
Qy 133 RRDTDCGTCPLGPFYEHGDCVCSTLGSQPE--RCAAVC 171  
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 155  
  
RESULT 9  
AAW52267  
ID AAW52267 standard; protein; 161 AA.  
XX  
AC AAW52267;  
XX  
XX 29-JUN-1998 (first entry)  
XX  
XX Soluble tumour necrosis factor receptor.  
XX  
XX Soluble tumour necrosis factor receptor; sTNFR; TNF-mediated disease;  
KW tumour necrosis factor binding protein; autoimmune disease; arthritis;  
KW adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;  
KW chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.  
XX  
XX

```
OS Homo sapiens.
PN WO9801555-A2.
XX
PD 15-JAN-1998.
XX
XX 09-JUL-1997; 97WO-US012244.
XX
XX 09-JUL-1996; 96US-0021443P.
PR 06-DEC-1996; 96US-0032534P.
PR 23-JAN-1997; 97US-0037737P.
PR 07-FEB-1997; 97US-0039314P.
PR 04-MAR-1997; 97US-0039792P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Fisher EF, Edwards CK, Kieft GL;
XX
XX WPI; 1998-101052/09.
DR N-PSDB; AAV19801.
XX
XX Truncated and soluble forms of tumour necrosis factor receptor - useful
PT for treating diseases involving factor, e.g. arthritis and adult
PT respiratory distress syndrome.
XX
XX Claim 1; Fig 1; 205pp; English.
XX
XX This sequence is the human soluble tumour necrosis factor receptor
CC (sTNFR). The protein was used to make the truncated sTNFR proteins of the
CC invention. The truncated sTNFR proteins and tumour necrosis factor
CC binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g.
CC arthritis, adult respiratory distress syndrome, cachexia/anorexia,
CC cancer, chronic fatigue syndrome, graft rejection, Alzheimer's disease
CC and other autoimmune diseases. Cells transformed with a vector containing
CC DNA encoding the protein may be used for production of recombinant sTNFR,
CC which may also be used for measuring the amount of sTNFR in samples and
CC to raise antibodies against sTNFR. TNBP may also be used in preparation
CC of therapeutic compositions for treating the above diseases. The sTNFR
CC proteins are well suited to large scale production (since they lack the
CC deamidation site in region 111-126, so are more stable in vivo); contain
CC fewer disulphide bonds and fewer epitopes, making them less antigenic
CC than full-length proteins
XX
XX Sequence 161 AA;
SQ
Query Match 19.3%; Score 200.5; DB 2; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.8e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 16 HKKIGLFCCRCGPAGHYLKAPCTPCGNGSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75
Db 11 HPQNNISICTKCHKGTLYNDCPGQDTCRECSGFTASENHLR-HCLSCSKCRKEM 69
Qy 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDGCALHRRHRLCS 132
Db 70 GQVEISSCTVDRDTCVCGCRKNQRYHWSLENLFCQ-----FNCSCLN-GTVH----LSCQ 119
Qy 133 RRDTCGTCCLPGFYEHGDCGVCSCPTSLGSCPE--RCAAVC 171
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 155
RESULT 10
AAW89233
ID AAW89233 standard; protein; 161 AA.
XX
AC AAW89233;
XX
XX 04-MAR-1999 (first entry)
XX
XX Tumour necrosis inhibitor 30 kDa protein.
XX
XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
```

```
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW inflammation; apoptosis.
XX
OS Homo sapiens.
XX
XX WO9849305-A1.
XX
XX 05-NOV-1998.
XX
XX 29-APR-1998; 98WO-US008631.
XX
XX 01-MAY-1997; 97US-00850188.
XX
XX (AMGE-) AMGEN INC.
XX
XX Boyle WJ, Wooden S;
XX
XX WPI; 1999-034661/03.
DR N-PSDB; AAV81732.
XX
XX New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin
PT dimerisation domain and a heterologous sequence, useful to treat TNF and
PT TNFR-mediated disorders.
XX
XX Disclosure; Fig 2; 92pp; English.
XX
XX The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are
CC used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents the TNF inhibitor 30 kDa protein
XX
XX Sequence 161 AA;
SQ
Query Match 19.3%; Score 200.5; DB 2; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.8e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 16 HKKIGLFCCRCGPAGHYLKAPCTPCGNGSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75
Db 11 HPQNNISICTKCHKGTLYNDCPGQDTCRECSGFTASENHLR-HCLSCSKCRKEM 69
Qy 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDGCALHRRHRLCS 132
Db 70 GQVEISSCTVDRDTCVCGCRKNQRYHWSLENLFCQ-----FNCSCLN-GTVH----LSCQ 119
Qy 133 RRDTCGTCCLPGFYEHGDCGVCSCPTSLGSCPE--RCAAVC 171
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 155
RESULT 11
AAB37676
ID AAB37676 standard; protein; 161 AA.
XX
AC AAB37676;
XX
XX 02-MAR-2001 (first entry)
XX
XX Human 30 kDa TNF inhibitor.
XX
XX TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW IL-1; inflammatory disease; degenerative disease; human.
```

```
XX OS Homo sapiens.
XX FN US6143866-A.
XX PD 07-NOV-2000.
XX PF 19-JAN-1995; 95US-00375242.
XX PR 18-JUL-1989; 89US-00381080.
XX PR 11-DEC-1989; 89US-00450329.
XX PR 07-FEB-1990; 90US-00479661.
XX PR 19-JUL-1990; 90US-00552274.
XX PR 09-JUL-1993; 93US-00090366.
XX PA (AMGE-) AMGEN INC.
XX PI Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
XX PI Vanderslice RW, Vannice J, Kohno T;
XX DR N-PSDB; AAC83945.
XX PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-
XX PT native cysteine residue cross-linked with polyethylene glycol, useful for
XX PT treating inflammatory and degenerative diseases mediated by TNF.
XX PS Claim 1; Fig 19; 82pp; English.
XX CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
XX CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
XX CC agents for inhibiting the activity of TNF and interleukin (IL-1), and for
XX CC treating inflammatory and degenerative diseases mediated by TNF. The 30
XX CC kDa TNF inhibitor can inhibit TNF alpha
XX SQ Sequence 161 AA;

Query Match 19.3%; Score 200.5; DB 4; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.8e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDQQA 75
DB 11 HPQNNISICTKCHKGTLYLNDPCGPGQDTCRECSGFTASENHLR-HCLSCSKCKREM 69
QY 76 SQVALENCASAVADTCGCKPGWFVEC---QVSQCVSSTPFCQPCLDGCGALHRRHLCS 132
DB 70 GQVEISSCTVDRDTCGCKRQYRHWSENLFQC-----FNCSLCLN-GTVH----LSCQ 119
QY 133 RRDTCGTCCLPGFYEHGDCVCSTPTSLGSCPE--RCAAVC 171
DB 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 155

RESULT 12
ABR62363
XX ID ABR62363 standard; protein; 161 AA.
XX AC ABR62363;
XX DT 22-SEP-2003 (first entry)
XX DE Tumour necrosis factor receptor extracellular domain.
XX KW Tumour necrosis factor; receptor; proline; protein engineering.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 23
XX FT Misc-difference 46 /note= "corresponds to wild-type His34 residue"
```

```
FT Misc-difference 76 /note= "corresponds to wild-type Ser57 residue"
FT FT /note= "corresponds to wild-type Ser87 residue"
XX PN WO2003046160-A2.
XX PD 05-JUN-2003.
XX PF 21-NOV-2002; 2002WO-EP013059.
XX PR 30-NOV-2001; 2001US-0340648P.
XX PA (ISTP ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX PI Brondyk W, Jiang X, Schweickhardt RL;
XX DR WPI; 2003-523245/49.
XX DR N-PSDB; ACC84134.
XX PT Increasing expression of a protein, comprises substituting at least one
XX PT codon in the polynucleotide encoding the protein, for a codon encoding
XX PT proline.
XX PS Disclosure; Fig 4; 53pp; English.
XX CC The present sequence is the protein sequence of the extracellular domain
XX CC of the p55 tumour necrosis factor receptor (TNFR). Screening of TNFR
XX CC mutant clones using a yeast display system yielded 2 mutant clones (see
XX CC ABR62364 and ABR62365) that showed higher expression levels in yeast than
XX CC in wild-type TNFR. The first clone contained a proline residue that
XX CC substituted the native Ser-87 residue (position 76 of the present
XX CC sequence). The other clone contain a proline residue that substituted the
XX CC native His-34 residue (23 of the present sequence) and also an isoleucine
XX CC residue that substituted the native Ile-57 residue (46 of the present
XX CC sequence) of TNFR. The invention provides methods of increasing protein
XX CC expression levels by substituting an amino acid residue with proline,
XX CC where the substitution occurs within 15 (preferably within 10, and
XX CC especially within 5) amino acids of a cysteine residue. The introduction
XX CC of proline residues may assist the polypeptide to adopt a favourable
XX CC conformation that fixes the neighbouring cysteine residue into the
XX CC correct orientation for disulfide bond formation, resulting in a higher
XX CC yield of correctly folded proteins in yeast or mammalian host cells
XX SQ Sequence 161 AA;

Query Match 19.3%; Score 200.5; DB 6; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.8e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDQQA 75
DB 11 HPQNNISICTKCHKGTLYLNDPCGPGQDTCRECSGFTASENHLR-HCLSCSKCKREM 69
QY 76 SQVALENCASAVADTCGCKPGWFVEC---QVSQCVSSTPFCQPCLDGCGALHRRHLCS 132
DB 70 GQVEISSCTVDRDTCGCKRQYRHWSENLFQC-----FNCSLCLN-GTVH----LSCQ 119
QY 133 RRDTCGTCCLPGFYEHGDCVCSTPTSLGSCPE--RCAAVC 171
DB 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 155

RESULT 13
ADA20577
XX ID ADA20577 standard; protein; 161 AA.
XX AC ADA20577;
XX DT 20-NOV-2003 (first entry)
XX DE Human 30kDa TNF inhibitor protein.
XX KW Human; tumour necrosis factor inhibitor; 30kDa TNF inhibitor;
```

KW 40kDa TNF inhibitor; TNF mediated pathological condition.

XX Homo sapiens.

PN US6541620-B1.

XX 01-APR-2003.

XX 07-JUN-1995; 95US-00484337.

XX 18-JUL-1989; 89US-00381080.

XX 11-DEC-1989; 89US-00450329.

XX 07-FEB-1990; 90US-00479661.

XX 19-JAN-1995; 95US-00375242.

XX (ANGE-) ANGEN INC.

PI Brewer MT, Thompson RC, Kohno T;

XX WPI; 2003-531100/50.

XX New nucleic acid comprising a sequence that encodes a polypeptide having

XX TNF inhibitory activity, useful for manufacturing a medicament for

XX treating a pathological condition mediated by TNF.

XX Example 2; Fig 19; 85pp; English.

XX The present invention relates to the isolation of novel human tumour

XX necrosis factor (TNF) inhibitor polypeptides (designated 30kDa TNF

XX inhibitor and 40kDa TNF inhibitor), and the polynucleotide sequences

XX encoding them. Also disclosed is a fragment of the 30kDa TNF inhibitor

XX polypeptide which comprises at least one non-native cysteine residue at

XX the N-terminus, C-terminus, residue 14 or preferably 105. The

XX polynucleotide sequence encoding the 30kDa TNF inhibitor is useful for

XX manufacturing a medicament for treating a pathological condition mediated

XX by TNF. The present sequence represents human 30kDa TNF inhibitor

XX protein.

XX Sequence 161 AA;

XX Query Match 19.3%; Score 200.5; DB 6; Length 161;

XX Best Local Similarity 29.8%; Pred. No. 1.8e-07;

XX Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWNHNSCARCQACDEQA 75

DB 11 HPQNNISCTCTKCHKGTLYNDPCPGQDTCRECESGSFTASENHLR-HCLSCSKCKREM 69

QY 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCS 132

DB 70 GQVEISSCTVDRDTRVCGCRKNQRYHWSENLFQC-----FNCSLCLN-GTVH----LSCQ 119

QY 133 RRDTDCGTCLPGFVEHGDGVCVCPSTLGSCEP---RCAAVC 171

DB 120 EKQNTVCTCHAGFLRENECVSC-----SNCKKSELECTKLC 155

RESULT 14

ADA20579

ID ADA20579 standard; protein; 161 AA.

XX ADA20579;

XX 20-NOV-2003 (first entry)

XX Human 30kDa TNF inhibitor protein.

XX Human; tumour necrosis factor inhibitor; 30kDa TNF inhibitor;

XX 40kDa TNF inhibitor; TNF mediated pathological condition.

XX Homo sapiens.

XX OS

XX PN US6541620-B1.

XX 01-APR-2003.

XX 07-JUN-1995; 95US-00484337.

XX 18-JUL-1989; 89US-00381080.

XX 11-DEC-1989; 89US-00450329.

XX 07-FEB-1990; 90US-00479661.

XX 19-JAN-1995; 95US-00375242.

XX (ANGE-) ANGEN INC.

XX Brewer MT, Thompson RC, Kohno T;

XX WPI; 2003-531100/50.

XX N-PSDB; ADA20578.

XX New nucleic acid comprising a sequence that encodes a polypeptide having

XX TNF inhibitory activity, useful for manufacturing a medicament for

XX treating a pathological condition mediated by TNF.

XX Claim 1; Fig 20; 85pp; English.

XX The present invention relates to the isolation of novel human tumour

XX necrosis factor (TNF) inhibitor polypeptides (designated 30kDa TNF

XX inhibitor and 40kDa TNF inhibitor), and the polynucleotide sequences

XX encoding them. Also disclosed is a fragment of the 30kDa TNF inhibitor

XX polypeptide which comprises at least one non-native cysteine residue at

XX the N-terminus, C-terminus, residue 14 or preferably 105. The

XX polynucleotide sequence encoding the 30kDa TNF inhibitor is useful for

XX manufacturing a medicament for treating a pathological condition mediated

XX by TNF. The present sequence represents human 30kDa TNF inhibitor

XX protein.

XX Sequence 161 AA;

XX Query Match 19.3%; Score 200.5; DB 6; Length 161;

XX Best Local Similarity 29.8%; Pred. No. 1.8e-07;

XX Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWNHNSCARCQACDEQA 75

DB 11 HPQNNISCTCTKCHKGTLYNDPCPGQDTCRECESGSFTASENHLR-HCLSCSKCKREM 69

QY 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCS 132

DB 70 GQVEISSCTVDRDTRVCGCRKNQRYHWSENLFQC-----FNCSLCLN-GTVH----LSCQ 119

QY 133 RRDTDCGTCLPGFVEHGDGVCVCPSTLGSCEP---RCAAVC 171

DB 120 EKQNTVCTCHAGFLRENECVSC-----SNCKKSELECTKLC 155

RESULT 15

ADH78698

ID ADH78698 standard; peptide; 161 AA.

XX ADH78698;

XX 15-APR-2004 (first entry)

XX Human tumour necrosis factor receptor 1 (TNF-R1) protein; SEQ ID No 106.

XX T-cell epitope; cytokine; receptor; CD4+; CD8+; immunogenicity;

XX interferon-beta; tumour necrosis factor receptor-1; erythropoietin;

XX thrombopoietin; inflammation; cancer; anaemia;

XX human tumour necrosis factor receptor 1; TNF-R1.

XX Homo sapiens.

XX OS

XX PN WO2003104263-A2.

XX 18-DEC-2003.

XX 26-FEB-2003; 2003WO-US005917.  
XX 01-MAY-2002; 2002US-0376743P.  
XX (GEMV ) GENENCOR INT INC.  
XX Harding FA, Power SD;  
XX WPI; 2004-062306/06.  
XX  
XX Determining T-cell epitope of a protein (e.g. cytokine or cytokine  
XX receptor); useful for reducing protein allergenicity, comprises combining  
XX differentiated dendritic cells and naive T-cells with a peptide having  
XX the T-cell epitope.  
XX  
XX Claim 4; SEQ ID NO 106; 51pp; English.  
XX  
XX The invention relates to a novel method for determining a T-cell epitope  
XX of a protein, where the protein is selected from cytokines and cytokine  
XX receptors. The method comprises combining a solution of differentiated  
XX dendritic cells and naive CD4+ and/or CD8+ T-cells with a pepset of  
XX peptides comprising the T-cell epitope. The composition and methods are  
XX useful in reducing the immunogenicity of cytokines and cytokine receptors  
XX such as interferon-beta, soluble tumour necrosis factor receptor-1,  
XX erythropoietin or thrombopoietin. These modified cytokines and cytokine  
XX receptors may be used for treating various conditions such as  
XX inflammation, cancer or anaemia. This sequence represents the human  
XX tumour necrosis factor receptor 1 (TNF-R1) protein of the invention.  
XX  
XX Sequence 161 AA;  
XX  
XX Query Match 19.3%; Score 200.5; DB 8; Length 161;  
XX Best Local Similarity 29.8%; Pred. No. 1.8e-07;  
XX Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
XX  
XX Qy 16 HKKIGLFCCRCPCAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECACQACDEQA 75  
XX Db 11 HPQNNSTCCTKCHRGTYLYNDPCPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69  
XX  
XX Qy 76 SQVALENCASAVADTRCGCKPGWFVEEC---QVSCVSSSPFYCQCLDCGALHRRHRLCS 132  
XX Db 70 GQVEISSCTVDRDTCGCRKNQYRHYSENLFQC-----FNCISCLN-GTVH----LSCQ 119  
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XX Qy 133 RRDTCGTCPLPGFYEHGDCGVCSPTSTLGSQCE--RCAAVC 171  
XX Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 155

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Job time : 163 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:19:32 ; Search time 158 Seconds  
(without alignments)

423.490 Million cell updates/sec

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Perfect score: 1038

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	210.5	20.3	162	9	US-09-798-789-12	Sequence 12, Appl
2	210.5	20.3	162	14	US-10-218-102-422	Sequence 422, App
3	205.5	19.8	162	9	US-09-798-789-13	Sequence 13, Appl
4	205.5	19.8	162	9	US-09-798-789-20	Sequence 20, Appl
5	205.5	19.8	162	14	US-10-218-102-423	Sequence 423, App
6	205.5	19.8	162	14	US-10-218-102-430	Sequence 430, App
7	203.5	19.6	162	9	US-09-798-789-11	Sequence 11, Appl
8	203.5	19.6	162	14	US-10-218-102-421	Sequence 421, App
9	203	19.6	173	9	US-09-899-429A-16	Sequence 16, Appl
10	201.5	19.4	162	9	US-09-798-789-19	Sequence 19, Appl
11	201.5	19.4	162	9	US-09-798-789-21	Sequence 21, Appl

12	201.5	19.4	162	14	US-10-218-102-429	Sequence 429, App
13	201.5	19.4	162	14	US-10-218-102-431	Sequence 431, App
14	200.5	19.3	153	9	US-09-800-909-3	Sequence 3, Appl
15	200.5	19.3	153	9	US-09-884-987-4	Sequence 4, Appl
16	200.5	19.3	153	9	US-09-800-908-12	Sequence 12, Appl
17	200.5	19.3	153	15	US-10-423-927-3	Sequence 3, Appl
18	200.5	19.3	153	16	US-10-632-929-12	Sequence 12, Appl
19	200.5	19.3	154	13	US-10-112-793-12	Sequence 12, Appl
20	200.5	19.3	154	15	US-10-375-680-53	Sequence 53, Appl
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22	200.5	19.3	161	9	US-09-907-263-2	Sequence 2, Appl
23	200.5	19.3	161	9	US-09-898-234-4	Sequence 4, Appl
24	200.5	19.3	161	9	US-09-899-429A-4	Sequence 4, Appl
25	200.5	19.3	161	9	US-09-792-356-4	Sequence 4, Appl
26	200.5	19.3	161	10	US-09-882-735-2	Sequence 2, Appl
27	200.5	19.3	161	14	US-10-436-826-73	Sequence 73, Appl
28	200.5	19.3	161	15	US-10-621-783-2	Sequence 2, Appl
29	200.5	19.3	161	15	US-10-622-383-2	Sequence 2, Appl
30	200.5	19.3	161	17	US-10-496-218-1	Sequence 1, Appl
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33	200.5	19.3	162	9	US-09-798-789-22	Sequence 22, Appl
34	200.5	19.3	162	9	US-09-899-429A-6	Sequence 6, Appl
35	200.5	19.3	162	14	US-10-218-102-419	Sequence 419, App
36	200.5	19.3	162	14	US-10-218-102-424	Sequence 424, App
37	200.5	19.3	162	14	US-10-218-102-432	Sequence 432, App
38	200.5	19.3	172	9	US-09-899-429A-20	Sequence 20, Appl
39	198.5	19.1	162	10	US-09-852-455-5	Sequence 5, Appl
40	196	18.9	139	10	US-09-405-032-126	Sequence 136, App
41	196	18.9	139	16	US-10-467-243-4	Sequence 4, Appl
42	194.5	18.7	162	9	US-09-798-789-10	Sequence 10, Appl
43	194.5	18.7	162	14	US-10-218-102-420	Sequence 420, App
44	193.5	18.6	162	9	US-09-798-789-17	Sequence 17, Appl
45	193.5	18.6	162	14	US-10-218-102-427	Sequence 427, App

ALIGNMENTS

RESULT 1  
US-09-798-789-12  
; Sequence 12 Application US/09798789  
; Patent No. US20020009780A1  
; GENERAL INFORMATION:  
; APPLICANT: Dahiyat, Bassil  
; APPLICANT: Filikov, Anton  
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA  
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED  
; TITLE OF INVENTION: DISORDERS  
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK  
; CURRENT APPLICATION NUMBER: US/09/798,789  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: US 60/186,427  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-798-789-12

Query Match	20.3%	Score 210.5;	DB 9;	Length 162;
Best Local Similarity	30.0%	Pred. No. 2.6e-09;		
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Db	12	HPQNNISCTCKHGKTYLNDPCGPGQDTCRECSGSFTASE-EHKRECLCSRCDKM	70	
Qy	76	SQVALENCSAVDTRCCKPGWFVECVSQVSSPPFYCQPCLCD--GALHHTRLCLSR	133	



Db 71 GQVEISSCTVDRDTCVCGCRKN-----QYRHYETENEFFCNCSLCLNGTVH-----LSCQE 121  
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## RESULT 2

US-10-218-102-422  
; Sequence 422, Application US/10218102  
; Publication No. US20030130827A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentzien, Joerg  
; APPLICANT: Dahiyat, Bassil I.  
; APPLICANT: Desjarlais, John R.  
; APPLICANT: Hayes, Robert J.  
; APPLICANT: Viglmetter, Jost  
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries  
; FILE REFERENCE: A-67229-11/RFT/RMS/RMK  
; CURRENT APPLICATION NUMBER: US/10/218,102  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: US 09/927,790  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/311,545  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: US 60/324,899  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/351,937  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/352,103  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 432  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 422  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-218-102-422

Query Match 20.3%; Score 210.5; DB 14; Length 162;  
Best Local Similarity 30.0%; Pred. No. 2.6e-09;  
Matches 48; Conservative 20; Mismatches 73; Indels 19; Gaps 6;

Qy 16 HKKIGLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQA 75  
Db 12 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECESGSFTASE-EHKRECLRCRCRDKM 70  
Qy 76 SOVALENCSAVADTRCGCKPGWFVECOVSQCVSSPFVQPCPLDC--GALHRHTRLCSR 133  
Db 71 GQVEISSCTVDRDTCVCGCRKN-----QYRHYETENEFFCNCSLCLNGTVH-----LSCQE 121  
Qy 134 RDTDCGTCLPGFYEHGDCVSCPTSTLGSQPE--RCAAVC 171  
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

## RESULT 3

US-09-798-789-13  
; Sequence 13, Application US/09798789  
; Patent No. US20020009780A1  
; GENERAL INFORMATION:  
; APPLICANT: Dahiyat, Bassil  
; APPLICANT: Filikov, Anton  
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA  
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED  
; TITLE OF INVENTION: DISORDERS  
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK  
; CURRENT APPLICATION NUMBER: US/09/798,789  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: US 60/186,427

; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-798-789-13

Query Match 19.8%; Score 205.5; DB 9; Length 162;  
Best Local Similarity 30.0%; Pred. No. 6.5e-09;  
Matches 48; Conservative 19; Mismatches 74; Indels 19; Gaps 6;  
Qy 16 HKKIGLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQA 75  
Db 12 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECESGSFTASENHLR-DCIQCSCQCKKHD 70  
Qy 76 SOVALENCSAVADTRCGCKPGWFVECOVSQCVSSPFVQPCPLDC--GALHRHTRLCSR 133  
Db 71 GQVEISSCTVDRDTCVCGCRKN-----QYRHYDHENRFYCNCSLCLNGTVH-----LSCQE 121  
Qy 134 RDTDCGTCLPGFYEHGDCVSCPTSTLGSQPE--RCAAVC 171  
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

## RESULT 4

US-09-798-789-20  
; Sequence 20, Application US/09798789  
; Patent No. US20020009780A1  
; GENERAL INFORMATION:  
; APPLICANT: Dahiyat, Bassil  
; APPLICANT: Filikov, Anton  
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA  
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED  
; TITLE OF INVENTION: DISORDERS  
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK  
; CURRENT APPLICATION NUMBER: US/09/798,789  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: US 60/186,427  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-798-789-20

Query Match 19.8%; Score 205.5; DB 9; Length 162;  
Best Local Similarity 30.4%; Pred. No. 6.5e-09;  
Matches 49; Conservative 20; Mismatches 71; Indels 21; Gaps 7;  
Qy 16 HKKIGLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQA 75  
Db 12 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECESGSFTASENHLR-HCLSCSKCRKEM 70  
Qy 76 SOVALENCSAVADTRCGCKPGWFVECO---VSQCVSSPFVQPCPLDCGALHRHTRLCS 132  
Db 71 GQVEISSCTVDRDTCVCGCRKNQYRHYOSENLFQC-----FNCISCLN-GTVH-----LSCQ 120  
Qy 133 RRTDCTCLPGFYEHGDCVSCPTSTLGSQPE--RCAAVC 171  
Db 121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

## RESULT 5

US-10-218-102-423  
; Sequence 423, Application US/10218102

```
; Publication No. US20030130827A1
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 09/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/352,103
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 423
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: synthetic
US-10-218-102-423

Query Match          19.8%; Score 205.5; DB 14; Length 162;
Best Local Similarity 30.0%; Pred. No. 6.5e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19; Gaps 6;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDQEA 75
Db 12 HPQNNISCTCKCHKGTLYLNDPCPGQDTCRECESGSFTASENHLR-DCLQCSQCKKHD 70

Qy 76 SOVALENCASAVADTRCGCKPGWFVEVCQ-----QYRHYDHENRFYCFNCSLCNLGTVH----LSCQE 121
Db 71 GQVEISSCTVDRTVCGCRKN-----QYRHYDHENRFYCFNCSLCNLGTVH----LSCQE 121

Qy 134 RDTDCGTCLPGFYEHGDCVSCPTSTLGSCE--RCAAVC 171
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

; RESULT 6
US-10-218-102-430
; Sequence 430, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 09/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/352,103
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 430
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: synthetic
US-10-218-102-430

Query Match          19.8%; Score 205.5; DB 14; Length 162;
Best Local Similarity 30.4%; Pred. No. 6.5e-09;
Matches 49; Conservative 20; Mismatches 71; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDQEA 75
Db 12 HPQNNISCTCKCHKGTLYLNDPCPGQDTCRECESGSFTASENHLR-HCLSCSKCKEM 70

Qy 76 SOVALENCASAVADTRCGCKPGWFVEVCQ---VSQVSSSPFYCQCLDCGALHRTLLCS 132
Db 71 GQVEISSCTVDRTVCGCRKNQYRHYQSENLFQC-----FNCISCLN-GTVH----LSCQ 120

Qy 133 RRTDTCGTCLPGFYEHGDCVSCPTSTLGSCE--RCAAVC 171
Db 121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

; RESULT 7
US-09-798-789-11
; Sequence 11, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 11
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-11

Query Match          19.6%; Score 203.5; DB 9; Length 162;
Best Local Similarity 30.0%; Pred. No. 9.3e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19; Gaps 6;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDQEA 75
Db 12 HPQNNISCTCKCHKGTLYLNDPCPGQDTCRECESGSFTASENHLRT-CLSCSKCKEM 70

Qy 76 SOVALENCASAVADTRCGCKPGWFVEVCQVSQVSSSPFYCQCLDC--GALHRTLLCSR 133
Db 71 GQVEISSCTVDRTVCGCRKN-----QYRHYASENKFQCFNCSLCNLGTVH----LSCQE 121

Qy 134 RDTDCGTCLPGFYEHGDCVSCPTSTLGSCE--RCAAVC 171
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

; RESULT 8
US-10-218-102-421
; Sequence 421, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 09/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/352,103
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 421
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-218-102-421

Query Match      19.6%; Score 203.5; DB 14; Length 162;
Best Local Similarity 30.0%; Pred. No. 9.3e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19; Gaps 6;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75
Db 12 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHRLT-CLSCSKCLKEM 70

Qy 76 SQVALENCASAVADTRCGCKPGWFVECVSQCVSSSPFYCQCLDC--GALHRRHRLTLCRSR 133
Db 71 GQVEISSCTVDRDTCVCGCRKN-----QYRHYASENKQCFNCSLCLNGTVH----LSCQE 121

Qy 134 RDTDCGTCLPGFYEHGDCVCSTPTSLGSCPE--RCAAVC 171
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 9
US-09-899-429A-16
; Sequence 16, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1955-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-Bp sequence
US-09-899-429A-16

Query Match      19.6%; Score 203; DB 9; Length 173;
Best Local Similarity 29.4%; Pred. No. 1.1e-08;
Matches 52; Conservative 20; Mismatches 81; Indels 24; Gaps 8;

Qy 3 GTRSPPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWEN 59
Db 7 GDREKRDVCPQGYIHPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASEN 66

Qy 60 HNSECARCOACDEQASQVALENCASAVADTRCGCKPGWFVECVSQCVSSSPFYCQ 116
Db 67 HLR-HCLSCSKCRKEMQVEISSCTVDRDTCVCGCRKNQYRHYASENLFQC-----FNCSL 120

Qy 117 CLDCGALHRRHRLTLCRRDTCGTCPLGFEYHGDGVCSTPTSLGSCPE--RCAAVC 171
Db 121 CLN-GTVH----LSCQEKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 167

RESULT 10
US-09-798-789-19
; Sequence 19, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-19

Query Match      19.4%; Score 201.5; DB 9; Length 162;
Best Local Similarity 29.8%; Pred. No. 1.3e-08;
Matches 46; Conservative 21; Mismatches 71; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75
Db 12 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHRL-HCLSCSKCRKEM 70

Qy 76 SQVALENCASAVADTRCGCKPGWFVECVSQCVSSSPFYCQCLDCGALHRRHRLTLCRS 132
Db 71 GQVEISSCTVDRDTCVCGCRKNQYRHYASENLFQC-----FNCSICLN-GTVH----LSCQ 120

Qy 133 RDTDCGTCLPGFYEHGDCVCSTPTSLGSCPE--RCAAVC 171
Db 121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 11
US-09-798-789-21
; Sequence 21, Application US/09798789
; Patent No. US20020009780A1
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```
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 21
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-21

Query Match      19.4%; Score 201.5; DB 9; Length 162;
Best Local Similarity 29.8%; Pred. No. 1.3e-08;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDFTFLAWENHNHSECARCQACDEQA 75
Db 12 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECESGSFTASENHLR-HCLGCSKCQKEM 70

Qy 76 SQVALENCASAVADTRCGCKPGWFVEQC---QVSCVSSSPFFYCQPCDLCGALHRRHRLCLS 132
Db 71 GQVEISSCTVDRDTCVCGCRKNQRYHNSENLFQC-----FNCSLCLN-GTVH----LSCQ 120

Qy 133 RRDTDGCTCLPGFYEHGDCVSCPTSTLGSCPE--RCAAVC 171
Db 121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 13
US-10-218-102-431
; Sequence 431, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 09/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/352,103
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 431
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-218-102-431

Query Match      19.4%; Score 201.5; DB 14; Length 162;
Best Local Similarity 29.8%; Pred. No. 1.3e-08;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDFTFLAWENHNHSECARCQACDEQA 75
Db 12 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECESGSFTASENHLR-HCLGCSKCQKEM 70

Qy 76 SQVALENCASAVADTRCGCKPGWFVEQC---QVSCVSSSPFFYCQPCDLCGALHRRHRLCLS 132
Db 71 GQVEISSCTVDRDTCVCGCRKNQRYHNSENLFQC-----FNCSLCLN-GTVH----LSCQ 120

Qy 133 RRDTDGCTCLPGFYEHGDCVSCPTSTLGSCPE--RCAAVC 171
Db 121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 14
US-09-800-909-3
; Sequence 3, Application US/09800909
; Patent No. US2001001983A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
US-10-218-102-429

Query Match      19.4%; Score 201.5; DB 14; Length 162;
```

APPLICANT: BIGDA, Jacek  
APPLICANT: BELETSKY, Igor  
APPLICANT: METT, Igor  
APPLICANT: ENGELMANN, Hartmut  
TITLE OF INVENTION: TNF INHIBITORS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/800,909  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,862  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 94039  
FILING DATE: 06-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 91229  
FILING DATE: 06-AUG-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 90339  
FILING DATE: 18-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=12A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 153 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-800-909-3

Query Match 19.3%; Score 200.5; DB 9; Length 153;  
Best Local Similarity 29.8%; Pred. No. 1.5e-08;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
Qy 16 HKKIGLFCCRGCPAGHYLKAPCTPCGNGSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75  
Db 9 HPQNNISICTCKCHKGTLYLNDPCPGQDTCRECESGSFTASENHLR-HCLSCSKCKREM 67  
Qy 76 SQVALENCNSAVADTRCGCKPGWFVEC---QVSQCVSPPFYCQPCLDGALHRRHRLCS 132  
Db 68 GQVEISSCTVDRDRTVCGCRKNQRYHWSNLFCQ-----FNCSLCLN-GTVH----LSCQ 117  
Qy 133 RRDTDCGTCLPGFVEHGDGCVSCPTSTLGSQPE--RCAAVC 171  
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSECTKLC 153

RESULT 15  
US-09-884-987-4  
; Sequence 4, Application US/09884987  
; Patent No. US202020102653A1  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu et al

TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN  
FILE REFERENCE: 0020-4877P  
CURRENT APPLICATION NUMBER: US/09/884,987  
CURRENT FILING DATE: 2001-06-21  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 153  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-884-987-4  
Query Match 19.3%; Score 200.5; DB 9; Length 153;  
Best Local Similarity 29.8%; Pred. No. 1.5e-08;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
Qy 16 HKKIGLFCCRGCPAGHYLKAPCTPCGNGSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75  
Db 9 HPQNNISICTCKCHKGTLYLNDPCPGQDTCRECESGSFTASENHLR-HCLSCSKCKREM 67  
Qy 76 SQVALENCNSAVADTRCGCKPGWFVEC---QVSQCVSPPFYCQPCLDGALHRRHRLCS 132  
Db 68 GQVEISSCTVDRDRTVCGCRKNQRYHWSNLFCQ-----FNCSLCLN-GTVH----LSCQ 117  
Qy 133 RRDTDCGTCLPGFVEHGDGCVSCPTSTLGSQPE--RCAAVC 171  
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSECTKLC 153

Search completed: June 27, 2005, 14:35:11  
Job time : 160 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:15:57 ; Search time 42 Seconds  
(without alignments)  
309.260 Million cell updates/sec

Title: US-10-081-280-6\_COPY\_25\_198

Perfect score: 1038  
Sequence: 1 QGTRSPRCAGDFHKKIG.....CPTSTLGSCEPACAAVCGWR 174

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 380303

Minimum DB seq length: 0  
Maximum DB seq length: 174

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCITUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200.5	19.3	153	2	US-08-219-237B-4
2	200.5	19.3	153	3	US-08-477-347-12
3	200.5	19.3	153	3	US-08-476-862-3
4	200.5	19.3	153	3	US-08-468-560C-4
5	200.5	19.3	153	4	US-09-800-909-3
6	200.5	19.3	153	4	US-09-800-908-12
7	200.5	19.3	154	4	US-08-828-683A-12
8	200.5	19.3	154	4	US-09-523-323-53
9	200.5	19.3	161	3	US-09-326-394-2
10	198.5	19.1	154	2	US-08-232-087A-10
11	196	18.9	139	3	US-08-706-945D-129
12	185	17.8	123	4	US-09-855-266A-13
13	182	17.5	155	3	US-09-146-950-4
14	182	17.5	159	3	US-09-146-950-20
15	181.5	17.5	161	4	US-09-523-323-56
16	170.5	16.4	158	1	US-08-050-319B-54
17	170.5	16.4	158	2	US-08-465-982-54
18	164.5	15.8	148	3	US-09-411-722-2
19	164.5	15.8	148	4	US-09-855-266A-2
20	162.5	15.7	119	2	US-08-219-237B-3
21	162.5	15.7	119	3	US-08-477-347-14
22	162.5	15.7	119	3	US-08-476-862-5
23	162.5	15.7	119	3	US-08-468-560C-3
24	162.5	15.7	119	4	US-08-828-683A-15
25	162.5	15.7	119	4	US-09-800-909-5
26	162.5	15.7	119	4	US-09-800-908-14
27	162.5	15.7	128	3	US-09-180-100-9

28	162.5	15.7	143	3	US-09-180-100-10	Sequence 10, Appl
29	162.5	15.7	144	3	US-09-180-100-21	Sequence 21, Appl
30	162.5	15.7	157	3	US-09-180-100-15	Sequence 15, Appl
31	162.5	15.7	159	3	US-09-180-100-23	Sequence 23, Appl
32	162.5	15.7	167	4	US-08-828-683A-22	Sequence 22, Appl
33	161	15.5	167	1	US-08-050-319B-2	Sequence 2, Appl
34	161	15.5	167	1	US-08-050-319B-57	Sequence 57, Appl
35	161	15.5	167	2	US-08-465-982-2	Sequence 2, Appl
36	161	15.5	167	2	US-08-465-982-57	Sequence 57, Appl
37	158.5	15.3	124	1	US-08-050-319B-4	Sequence 4, Appl
38	158.5	15.3	124	2	US-08-465-982-4	Sequence 4, Appl
39	155.5	15.0	133	4	US-09-612-033B-6	Sequence 6, Appl
40	152.5	14.7	157	1	US-08-050-319B-50	Sequence 50, Appl
41	152.5	14.7	157	2	US-08-465-982-50	Sequence 50, Appl
42	141.5	13.6	170	4	US-09-523-323-57	Sequence 57, Appl
43	140.5	13.5	170	4	US-08-828-683A-14	Sequence 14, Appl
44	136	13.1	162	2	US-08-219-237B-7	Sequence 7, Appl
45	136	13.1	162	3	US-08-477-347-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-219-237B-4  
; Sequence 4, Application US/08219237B  
; Patent No. 5874546  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu  
; APPLICANT: ITOH, Naoto  
; APPLICANT: YONEHARA, Shin  
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James W. Hellwege  
; STREET: P.O. Box 2266 Eads Station  
; City: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/219,237B  
; FILING DATE: 28-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/872,129  
; FILING DATE: 22-APR-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James W. Hellwege  
; REGISTRATION NUMBER: 28,808  
; REFERENCE/DOCKET NUMBER: 516762  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 153 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-219-237B-4

Query Match 19.3%; Score 200.5; DB 2; Length 153;  
Best Local Similarity 23.8%; Pred. No. 7.7e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
Oy 16 HKKIGLFCRCGCPAGHYLKAPCTPCGNCSTCLVQPDFTFLAWNHHSNCAACQACDQQA 75  
Db 9 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKKEM 67



Db 118 EKQNTVCTCHAGFFLURENECVSC-----SNCKKSLECTKLC 153

RESULT 4

US-08-468-560C-4

; Sequence 4, Application US/08468560C

; Patent No. 6270998

; GENERAL INFORMATION:

; APPLICANT: NAGATA, Shigekazu

; APPLICANT: ITOH, Naoto

; APPLICANT: YONEHARA, Shin

; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE

; TITLE OF INVENTION: ANTIGEN

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.

; STREET: P.O. BOX 747

; CITY: FALLS CHURCH

; STATE: VA

; COUNTRY: USA

; ZIP: 22040-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468.560C

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MURPHY JR., GERLAD M.

; REGISTRATION NUMBER: 28,977

; REFERENCE/DOCKET NUMBER: 20-4393P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-205-8000

; TELEFAX: 703-205-8050

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 153 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-468-560C-4

Query Match 19.3%; Score 200.5; DB 3; Length 153;

Best Local Similarity 29.8%; Pred. No. 7.7e-11;

Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDQQA 75

Db 9 HPQNNISCTCKHGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 67

Qy 76 SQVALENCASAVADTRCGCKPGWFVEC-----QVSQCVSPPFYCQPCDCLGALHRRHRLCS 132

Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHWYSENLFQC-----FNCSCLN-GTVH-----LSCQ 117

Qy 133 RRDTDCGTLCPGFYEHGDCVCSTSLGSCPE--RCAAVC 171

Db 118 EKQNTVCTCHAGFFLURENECVSC-----SNCKKSLECTKLC 153

RESULT 5

US-09-800-909-3

; Sequence 3, Application US/09800909

; Patent No. 655111

; GENERAL INFORMATION:

; APPLICANT: WALLACH, David

; APPLICANT: BIGDA, Jacek

; APPLICANT: BELETSKY, Igor

; APPLICANT: METT, Igor

; APPLICANT: ENGELMANN, Hartmut

; TITLE OF INVENTION: TNF INHIBITORS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/800.909

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/476,862

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 94039

; FILING DATE: 06-APR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 91229

; FILING DATE: 06-AUG-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 90339

; FILING DATE: 18-MAY-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: WALLACH=12A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 153 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-800-909-3

Query Match 19.3%; Score 200.5; DB 4; Length 153;

Best Local Similarity 29.8%; Pred. No. 7.7e-11;

Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDQQA 75

Db 9 HPQNNISCTCKHGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 67

Qy 76 SQVALENCASAVADTRCGCKPGWFVEC-----QVSQCVSPPFYCQPCDCLGALHRRHRLCS 132

Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHWYSENLFQC-----FNCSCLN-GTVH-----LSCQ 117

Qy 133 RRDTDCGTLCPGFYEHGDCVCSTSLGSCPE--RCAAVC 171

Db 118 EKQNTVCTCHAGFFLURENECVSC-----SNCKKSLECTKLC 153

RESULT 6

US-09-800-908-12

; Sequence 12, Application US/09800908

; Patent No. 6602993

; GENERAL INFORMATION:

; APPLICANT: WALLACH, David

; APPLICANT: BIGDA, Jacek

; APPLICANT: BELETSKY, Igor

; APPLICANT: METT, Igor

; TITLE OF INVENTION: TNF LIGANDS



NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/800,908  
FILING DATE: 08-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,347  
FILING DATE: <Unknown>  
APPLICATION NUMBER: IL 106271  
FILING DATE: 08-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, G. Kevin  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: WALLACH=10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 12:  
Best Local Similarity 29.8%; Score 200.5; DB 4; Length 153;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 153 amino acids  
STYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-800-908-12  
Query Match 19.3%; Score 200.5; DB 4; Length 153;  
Best Local Similarity 29.8%; Pred. No. 7.7e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
Qy 16 HKKIGLFCRCGPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75  
Db 9 HPQNNISCTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHRL-HCLSCSKCKREM 67  
Qy 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSCVSSSPFYCQPCLDGALHRRHRLTLLCS 132  
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQC-----FNCSICLN-GTVH----LSCQ 117  
Qy 133 RRDTCGTCCLPGFVHGDCGVCSTPTSLGSCPE--RCAAVC 171  
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 153  
RESULT 7  
US-08-828-683A-12  
Sequence 12, Application US/08828683A  
Patent No. 6469144  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,683A  
FILING DATE: 31-Mar-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/625328  
FILING DATE: 1-Apr-1996  
APPLICATION NUMBER: 08/710802  
FILING DATE: 23-Sep-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1007P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-08-828-683A-12  
Query Match 19.3%; Score 200.5; DB 4; Length 154;  
Best Local Similarity 29.8%; Pred. No. 7.7e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
Qy 16 HKKIGLFCRCGPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75  
Db 9 HPQNNISCTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHRL-HCLSCSKCKREM 67  
Qy 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSCVSSSPFYCQPCLDGALHRRHRLTLLCS 132  
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQC-----FNCSICLN-GTVH----LSCQ 117  
Qy 133 RRDTCGTCCLPGFVHGDCGVCSTPTSLGSCPE--RCAAVC 171  
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 153  
RESULT 8  
US-09-523-323-53  
Sequence 53, Application US/09523323  
Patent No. 6635743  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ruben, Steven M.  
APPLICANT: Ullrich, Stephen  
APPLICANT: Zhai, Yifan  
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
FILE REFERENCE: 1488.065000C  
CURRENT APPLICATION NUMBER: US/09/523,323  
CURRENT FILING DATE: 2000-03-10  
EARLIER APPLICATION NUMBER: 60/168,380  
EARLIER FILING DATE: 1999-12-02  
EARLIER APPLICATION NUMBER: 60/148,326  
EARLIER FILING DATE: 1999-08-11  
EARLIER APPLICATION NUMBER: 60/142,657  
EARLIER FILING DATE: 1999-07-06  
EARLIER APPLICATION NUMBER: 60/137,457  
EARLIER FILING DATE: 1999-06-04  
EARLIER APPLICATION NUMBER: 60/124,041  
EARLIER FILING DATE: 1999-03-11  
EARLIER APPLICATION NUMBER: 09/252,656  
EARLIER FILING DATE: 1999-02-19  
EARLIER APPLICATION NUMBER: 60/075,409  
EARLIER FILING DATE: 1998-02-20

EARLIER APPLICATION NUMBER: 09/027,287  
EARLIER FILING DATE: 1998-02-20  
EARLIER APPLICATION NUMBER: 09/003,886  
EARLIER FILING DATE: 1998-01-07  
EARLIER APPLICATION NUMBER: 08/822,953  
EARLIER FILING DATE: 1997-03-21  
EARLIER APPLICATION NUMBER: 60/013,923  
EARLIER FILING DATE: 1996-03-22  
EARLIER APPLICATION NUMBER: 60/030,157  
EARLIER FILING DATE: 1996-10-31  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 53  
LENGTH: 154  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-523-323-53

Query Match 19.3%; Score 200.5; DB 4; Length 154;  
Best Local Similarity 29.8%; Pred. NO. 7.7e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
Qy 16 HKKIGLFCRCPCAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQEA 75  
Db 9 HPQNSICTCKHGTLYNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCKREM 67  
Qy 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDCLGALHHRHRLICS 132  
Db 68 GQVEISSCTVDRTVCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GTVH---LSCQ 117  
Qy 133 RRDTCGTCLPGFVGHGDCVSCPTSTLGSCE--RCAAVC 171  
Db 118 EKQNTVCTCHAGFFLENECVSC-----SNCKKSLECTKLC 153

RESULT 9  
US-09-326-394-2  
Sequence 2, Application US/09326394  
Patent No. 6306820  
GENERAL INFORMATION:  
APPLICANT: Bendele, Alison M.  
APPLICANT: Sennello, Regina M.  
APPLICANT: Edwards, Carl K.  
TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 DeHavilland Drive  
CITY: Thousand Oaks  
STATE: CA  
COUNTRY: US  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/326,394  
FILING DATE: 08-DEC-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/032,587  
FILING DATE: 06-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,355  
FILING DATE: 23-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,315  
FILING DATE: 07-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/052,023

FILING DATE: 09-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Zindrick, Thomas K.  
REGISTRATION NUMBER: 32,185  
REFERENCE/DOCKET NUMBER: A-430D  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-326-394-2

Query Match 19.3%; Score 200.5; DB 3; Length 161;  
Best Local Similarity 29.8%; Pred. NO. 8.1e-11;  
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;  
Qy 16 HKKIGLFCRCPCAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQEA 75  
Db 11 HPQNSICTCKHGTLYNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCKREM 69  
Qy 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDCLGALHHRHRLICS 132  
Db 70 GQVEISSCTVDRTVCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GTVH---LSCQ 119  
Qy 133 RRDTCGTCLPGFVGHGDCVSCPTSTLGSCE--RCAAVC 171  
Db 120 EKQNTVCTCHAGFFLENECVSC-----SNCKKSLECTKLC 155

RESULT 10  
US-08-232-087A-10  
Sequence 10, Application US/08232087A  
Patent No. 5866372  
GENERAL INFORMATION:  
APPLICANT: Stein, Harald  
APPLICANT: D rkoop, Horst  
APPLICANT: Latza, Ute  
TITLE OF INVENTION: Lymphoid CD30-Antigen  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
STREET: 8110 Gatehouse Road, Suite 500 East  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22042  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,087A  
FILING DATE: 08-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 756-103P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal

```
;
;
; NAME/KEY: Protein
; LOCATION: 1..154
; OTHER INFORMATION: /note= "TNF1, see Fig. 5"
US-08-232-087A-10

Query Match      19.1%; Score 198.5; DB 2; Length 154;
Best Local Similarity 30.4%; Pred. No. 1.2e-10;
Matches 49; Conservative 23; Mismatches 68; Indels 21; Gaps 8;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQA 75
Db 9 HPQNNISCTTKCHKGTYLYNDPCPGQDTCDECSQSFTASENHLR-HCLSCSKCKREM 67
Qy 76 SQVALENCASAVADTRCGCKPGWFVEVC---QVSQCVSSSPFYCQPCLDGCGALHRRHRLCS 132
Db 68 GQVEISSCTVDRDVTGCGCKNQRYHYSNLFQC-----FNCSICLN-GTVHLSGQ---E 118
Qy 133 RRDDTCGTCLPGFYEHGDCVSCPTSTLGSCE--RCAAVC 171
Db 119 KQNTVC-TCHAGFFLENECVSC-----GNCKSLECTKLC 153

RESULT 11
US-08-706-945D-129
; Sequence 129, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; CURRENT FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-706-945D-129

Query Match      18.9%; Score 196; DB 3; Length 139;
Best Local Similarity 31.5%; Pred. No. 1.8e-10;
Matches 45; Conservative 17; Mismatches 67; Indels 14; Gaps 5;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQA 75
Db 8 HPQNNISCTTKCHKGTYLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 66
Qy 76 SQVALENCASAVADTRCGCKPGWFVEVC---QVSQCVSSSPFYCQPCLDGCGALHRRHRLCS 132
Db 67 GQVEISSCTVDRDVTGCGCKNQRYHYSNLFQC-----FNCSICLN-GTVH----LSCQ 116
Qy 133 RRDDTCGTCLPGFYEHGDCVSC 155
Db 117 EKQNTVCTCHAGFFLENECVSC 139

RESULT 12
US-09-855-266A-13
; Sequence 13, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 08501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
```

```
;
;
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-13

Query Match      17.8%; Score 185; DB 4; Length 123;
Best Local Similarity 28.8%; Pred. No. 1.5e-09;
Matches 47; Conservative 16; Mismatches 58; Indels 42; Gaps 6;

Qy 11 CAGD--FHKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARC 68
Db 1 CPGKYVHSKNNISCTTKCHKGYLYSDCSPGRDTCRECEKGTFTASQNYLR-QCLSC 59
Qy 69 QACDEQASQVALENCASAVADTRCGCKPGWFVEVCQVSQCVSSSPFYCQPCLDGCGALHRRH 128
Db 60 KTCRKEMSQVEISPCQADKDTVCCK-----ENQFQRYLSETHQC----- 100
Qy 129 LLCRRDTCGTCLPGFYEHGDCVSCPTSTLGSCEPCCAIVC 171
Db 101 -----VDCSPCF-----NGTVTIP-----CKETONTVC 123

RESULT 13
US-09-146-950-4
; Sequence 4, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-4

Query Match      17.5%; Score 182; DB 3; Length 155;
Best Local Similarity 30.7%; Pred. No. 3.6e-09;
Matches 46; Conservative 14; Mismatches 66; Indels 24; Gaps 6;

Qy 19 IGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNH--SECARQACDEQAS 76
Db 11 VGSECCPKCSFGYRVKACGELTG-TVCEPCPGCTIYA---HLNGLSKLCCQCMCDPAMG 66
Qy 77 QVALENCASAVADTRCGCKPGWFVEVCQVSQCVSSSPFYCQPCLDGCGALHRRHRL---CSR 133
Db 67 LRASRNCSTENAVCGCSPGHF-----CIVQGDHCAACRAYATSSPGQVQKGGTES 119
Qy 134 RDTDCGTCLPGFYEHGDCVSCPTSTLGS 163
Db 120 QDTLCQNCPPGTFS-----PNTLEEC 141

RESULT 14
US-09-146-950-20
; Sequence 20, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
```

```
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-20

Query Match      17.5%; Score 182; DB 3; Length 159;
Best Local Similarity 30.1%; Pred. No. 3.7e-09;
Matches 46; Conservative 14; Mismatches 66; Indels 24; Gaps 6;

Qy  19 IGLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNH--SECARCOACDEQAS 76
Db  11 VGSECCPKCSPGYRVKEACGELTG-TVCEPCPPGTYTA---HLNGLSKCLQCQMCDPAMG 66

Qy  77 QVALENCASAVADTRCGCKPGWFVECVSQVSSPFFVYQPCDCLDCGALHRRHRL--CSR 133
Db  67 LRASRNCSTENAVCGSPGHF-----CIVQGDHCAACRAYATSSPGQRVQKGGTES 119

Qy  134 RDTDCGTCLPGFYEHGDCVSCPTSTLWSC 163
Db  120 QDTLCQNCPPGTFS-----PNTLLEC 141
```

```
RESULT 15
US-09-523-323-56
; Sequence 56, Application US/09523323
; Patent No. 6635743
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ulrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065000C
; CURRENT APPLICATION NUMBER: US/09/523,323
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/168,380
; EARLIER FILING DATE: 1999-12-02
; EARLIER APPLICATION NUMBER: 60/148,326
; EARLIER FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/142,657
; EARLIER FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 60/137,457
; EARLIER FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: 60/124,041
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 09/252,656
; EARLIER FILING DATE: 1999-02-19
; EARLIER APPLICATION NUMBER: 60/075,409
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/027,287
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: 60/013,923
; EARLIER FILING DATE: 1996-03-22
; EARLIER APPLICATION NUMBER: 60/030,157
; EARLIER FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 161
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-523-323-56

Query Match      17.5%; Score 181.5; DB 4; Length 161;
Best Local Similarity 30.1%; Pred. No. 4.1e-09;
Matches 49; Conservative 14; Mismatches 67; Indels 33; Gaps 8;

Qy  19 IGLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNH--SECARCOACDEQAS 76
Db  9 VGSECCPKCSPGYRVKEACGELTG-TVCEPCPPGTYTA---HLNGLSKCLQCQMCDPAMG 64

Qy  77 QVALENCASAVADTRCGCKPGWFVECVSQVSSPFFVYQPCDCLDCGAL-----HRRHRL 130
Db  65 LRASRNCSTENAVCGSPGHF-----CIVQGDHCA-----CRAYATSSPGQRVQKSG 113

Qy  131 CSRRTDCGTCLPGFYEHGDCVSCPTSTLWSCPERCAAVCGW 173
Db  114 TESQDTLCQNCPPGTFS-----PNTLLECQHQ--TKCSW 146

Search completed: June 27, 2005, 14:31:21
Job time : 43 secs
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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	52.5	12.7	74	2	F71080	hypothetical prote
2	50.5	12.2	71	2	G69463	conserved hypothet
3	50.5	12.2	72	2	E63386	hypothetical prote
4	50.5	12.2	73	2	D69499	conserved hypothet
5	50.5	12.2	79	2	A84092	hypothetical prote
6	49.5	12.0	78	2	H84353	hypothetical prote
7	48	11.6	72	2	A82881	conserved hypothet
8	47	11.4	60	2	D83610	hypothetical prote
9	47	11.4	61	2	C69373	hypothetical prote
10	47	11.4	67	2	A96702	unknown protein, 7
11	46.5	11.3	64	2	G83940	hypothetical prote
12	46.5	11.3	68	2	JH0129	repressor protein
13	46.5	11.3	79	2	AH0619	probable damage-in
14	46	11.1	72	2	A75099	hypothetical prote
15	46	11.1	76	2	H70576	hypothetical prote
16	45.5	11.0	52	2	F83985	hypothetical prote
17	45	10.9	67	2	AC1037	probable phage tai
18	45	10.9	71	1	H70799	glutathione-related
19	45	10.9	80	2	F72303	glutaredoxin - The
20	44.5	10.8	72	2	G91153	host factor for ly
21	44.5	10.8	72	2	C85999	host factor for ly
22	44.5	10.8	72	2	A49988	slx protein - Esc
23	44.5	10.8	74	2	B75199	hypothetical prote
24	44	10.7	67	2	AG0927	probable phage tai
25	44	10.7	68	2	B55682	keratin 15, type I
26	44	10.7	70	2	F81899	hypothetical prote
27	43.5	10.5	62	2	F69871	hypothetical prote
28	43.5	10.5	75	2	AE2659	conserved hypothet
29	43.5	10.5	75	2	C97441	hypothetical prote



A:Gene: UU518

A:Genetic code: SGC3

Query Match

Best Local Similarity 28.0%; Score 48; DB 2; Length 72;

Matches 7; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 12 EFVRLTGLREAEIEAVEVEIGRFRD 36

DB 41 EYIKTLGRNQNAVVIQTKDGKFD 65

RESULT 8

DB3610

hypotheical protein PA0284 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C&gt;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

R:Accession: D83610

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: D83610

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-60 &lt;STO&gt;

A:Cross-references: UNIPROT:Q916K6; GB:AE004466; GB:AE004091; NID:g9946120; PIDN:AAG0367

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0284

Query Match

Best Local Similarity 36.4%; Score 47; DB 2; Length 60;

Matches 12; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 19 LREAEIEAVEIGRFRDQOQYEMLRKRWQQA 51

DB 24 LRGLRFGAVEITVHGQVQVIERKEKRLQQA 56

RESULT 9

C69333

hypotheical protein AF0667 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C&gt;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

R:Accession: C69333

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: C69333

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-61 &lt;KLE&gt;

A:Cross-references: UNIPROT:Q29590; GB:AE001058; GB:AE000782; NID:g2689381; PIDN:AAB9057

Query Match

Best Local Similarity 34.5%; Score 47; DB 2; Length 61;

Matches 10; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 35 RQOQYEMLRKRWQQAQAGVYALERM 63

DB 31 RDEKRLMLERMRDELEAELEIKRBIERL 59

RESULT 10

A96702

unknown protein, 70659-70456 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C&gt;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

R:Accession: A96702

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A96702

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-87 &lt;STO&gt;

A:Cross-references: UNIPROT:Q9C9V8; GB:AE005173; NID:g6553903; PIDN:AAF16569.1; GSPDB:GN

C:Genetics:

A:Gene: T23K23.23

A:Map position: 1

Query Match

Best Local Similarity 34.8%; Score 47; DB 2; Length 67;

Matches 16; Conservative 5; Mismatches 13; Indels 12; Gaps 2;

QY 11 KEF--VRTLGLREAEIEAVEVEIGRFRDQOQYEMLRKRWQQAQAGLG 54

DB 24 KEFEKIQPSLQPEMRRLVSEIKR-----RQSRSPPLGLG 59

RESULT 11

GB3940

hypotheical protein BH2327 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C&gt;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

R:Accession: GB3940

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: GB3940

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-64 &lt;STO&gt;

A:Cross-references: UNIPROT:Q9KAG0; GB:AP001515; GB:BA000004; NID:gl0174886; PIDN:BA0604

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH2327

Query Match

Best Local Similarity 31.8%; Score 46.5; DB 2; Length 64;

Matches 14; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

QY 19 LREAEIEAVEVE-----IGRFRDQOQYEMLRKRWQQAQAGLV 57

DB 13 LRDELESVRIEKNDFLIFRQVLAEQEDMKSFGRGNAQRGGGVY 56

RESULT 12

JH0129

repressor protein cac - Escherichia coli plasmid RSP1010

N:Alternate names: repressor protein P

C:Species: Escherichia coli

A:Note: plasmid RSP1010 is a broad-host-range plasmid belonging to incompatibility group

C&gt;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004

R:Accession: JH0129; PS0292

R:Scholz, P.; Haring, V.; Wittmann-Liebold, B.; Ashman, K.; Bagdasarian, M.; Scherzinger,

Gene 75, 271-288, 1989

A:Title: Complete nucleotide sequence and gene organization of the broad-host-range plasm

A:Reference number: JH0123; MUID:89232758; PMID:2653965



A;Accession: JH0129  
A:Molecule type: DNA  
A;Residues: 1-68 <SCH1>  
A;Cross-references: UNIPROT.Q52350; GB:M28829; NID:g152577; PIDN:AAA26449.1; PID:g152569S

C;Comment: This protein binds to the operator region of a promoter located at upstream d  
C;Genetics:  
A;Gene: cac  
A;Genome: plasmid

Query Match            11.3%; Score 46.5; DB 2; Length 68;  
Best Local Similarity 20.8%; Pred.No.3.e+02;  
Matches 15; Conservative 11; Mismatches 15; Indels 31; Gaps 2;

QY      3 DAVPARWKKEFVTLGLREAEIEAVEVEIGRFDDQQEMLKRWROQPAGLGAVYAALER 62  
     ||| : : : | : : : : : : :  
Db     17 DA VRGARYERMKAKGMQRKF-----WLTDEYEALR----- 50  
     |:| :| :|| :

QY      63 MGLDGCVCVELRS 74  
     |:| :| :|| :

Db     51 -----CLEELRA 57  
     |:| :| :|| :

RESULT 13  
AH0619  
probable damage-inducible protein STY1032 [imported] - Salmonella enterica subsp. enteric  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AH0619  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
., S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A;Reference number: AB0502; UID:21534947; PMID:11677608  
A;Accession: AH0619  
A>Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-79 <PAP>  
A;Cross-references: GB:AL513382; PIDN:CAD05426.1; PID:g16502187; GSFPDB:GN00176  
C;Genetics:  
A;Gene: STY1032

Query Match            11.3%; Score 46.5; DB 2; Length 79;  
Best Local Similarity 32.8%; Pred.No.3.9e+02;  
Matches 22; Conservative 8; Mismatches 24; Indels 13; Gaps 3;

QY      15 RTLGLREAEIEAVEVEIGRFDDQQE----MLKRWROQPAGLGAVYAALERMGDCCVE 70  
     ||| : : : | : : : : : : :  
Db     9 RTKLPGEGPALEKELITRLQNQYNCLTIRGSOD---GLSIVGA--DGDKX 59  
     ||| :| :|| :

QY      71 DLRSRLQ 77  
     :| :|| :

Db      60 RIQSILQ 66  
     :| :|| :

RESULT 14  
A75099  
hypothetical protein PAB3293 - Pyrococcus abyssi (strain Orsay)  
C;Species: Pyrococcus abyssi  
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: A75099  
R;anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str  
A;Reference number: A75001  
A;Accession: A75099  
A>Status: preliminary  
A:Molecule type: DNA

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2005, 14:30:44 ; Search time 168 Seconds  
(without alignments) 243.847 Million cell u

**Title:** US-10-081-280-6 COPY 338 417

Perfect score: 413  
Sequence: 1 VMDAVPARRWKEFVRTLGLR.....ERMGLDGCVEDLRSLRQGP 80

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 164759

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Minimum DB seq length: 0
Maximum DB seq length: 80
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 458

Database : UniProt 03:★

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1: uniprot_sprot:*
2: uniprot_trembl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	59	14.3	79	2	Q93R97 pseudomonas
2	57	13.8	55	2	Q6TG30 azomonas ma
3	54.5	13.2	59	2	Q7P3Z1 fusobacteri
4	54	13.1	69	2	Q9ZXL9 bacterioph
5	54	13.1	78	2	Q6CZU0 erwinia car
6	53.5	13.0	79	2	Q8TYA5 methanopyru
7	53	12.8	62	2	Q72GH9 thermus the
8	53	12.8	75	2	Q8U397 pyrococcus
9	53	12.8	78	2	Q7U9X2 synethococc
10	52.5	12.7	70	2	Q8H4R5 oryza sativ
11	52.5	12.7	74	2	Q73992 pyrococcus
12	52.5	12.7	77	2	Q6PX4Y staphylococ
13	52	12.6	70	2	Q93NF5 arthrobacte
14	51	12.3	66	2	Q88AU2 pseudomonas
15	50.5	12.2	62	2	Q7EYN4 oryza sativ
16	50.5	12.2	70	2	Q7W7D7 prochlorococ
17	50.5	12.2	71	1	YH12_ARCFU
18	50.5	12.2	72	1	YA94_ARCFU
19	50.5	12.2	73	1	YJ97_ARCFU
20	50.5	12.2	79	2	Q9K736 bacillus ha
21	50	12.1	61	2	Q8DD62 vibrio vuln
22	50	12.1	63	2	Q9MX53 ginglymosto
23	50	12.1	66	2	Q8ECW2 shewanella
24	50	12.1	72	2	Q87PB4 vibrio para
25	49.5	12.0	78	2	Q9HNM4 halobacteri
26	49	11.9	54	2	Q6K5Y5 oryza sativ
27	49	11.9	72	2	Q7MKX6 vibrio vuln
28	49	11.9	72	2	Q8D9G2 vibrio vuln
29	48.5	11.7	51	2	Q8CA05 mus musculu
30	48.5	11.7	60	2	Q883A4 pseudomonas
31	48.5	11.7	71	2	Q716N0 mycobacteri

	32	48	60	72	84	96	108	120	132	144	156	168	180	192	204	216	228	240	252	264	276	288	300	312	324	336	348	360	372	384	396	408	420	432	444	456	468	480	492	504	516	528	540	552	564	576	588	600	612	624	636	648	660	672	684	696	708	720	732	744	756	768	780	792	804	816	828	840	852	864	876	888	900	912	924	936	948	960	972	984	996	1008	1020	1032	1044	1056	1068	1080	1092	1104	1116	1128	1140	1152	1164	1176	1188	1200	1212	1224	1236	1248	1260	1272	1284	1296	1308	1320	1332	1344	1356	1368	1380	1392	1404	1416	1428	1440	1452	1464	1476	1488	1500	1512	1524	1536	1548	1560	1572	1584	1596	1608	1620	1632	1644	1656	1668	1680	1692	1704	1716	1728	1740	1752	1764	1776	1788	1800	1812	1824	1836	1848	1860	1872	1884	1896	1908	1920	1932	1944	1956	1968	1980	1992	2004	2016	2028	2040	2052	2064	2076	2088	2100	2112	2124	2136	2148	2160	2172	2184	2196	2208	2220	2232	2244	2256	2268	2280	2292	2304	2316	2328	2340	2352	2364	2376	2388	2400	2412	2424	2436	2448	2460	2472	2484	2496	2508	2520	2532	2544	2556	2568	2580	2592	2604	2616	2628	2640	2652	2664	2676	2688	2700	2712	2724	2736	2748	2760	2772	2784	2796	2808	2820	2832	2844	2856	2868	2880	2892	2904	2916	2928	2940	2952	2964	2976	2988	3000	3012	3024	3036	3048	3060	3072	3084	3096	3108	3120	3132	3144	3156	3168	3180	3192	3204	3216	3228	3240	3252	3264	3276	3288	3300	3312	3324	3336	3348	3360	3372	3384	3396	3408	3420	3432	3444	3456	3468	3480	3492	3504	3516	3528	3540	3552	3564	3576	3588	3600	3612	3624	3636	3648	3660	3672	3684	3696	3708	3720	3732	3744	3756	3768	3780	3792	3804	3816	3828	3840	3852	3864	3876	3888	3900	3912	3924	3936	3948	3960	3972	3984	3996	4008	4020	4032	4044	4056	4068	4080	4092	4104	4116	4128	4140	4152	4164	4176	4188	4200	4212	4224	4236	4248	4260	4272	4284	4296	4308	4320	4332	4344	4356	4368	4380	4392	4404	4416	4428	4440	4452	4464	4476	4488	4500	4512	4524	4536	4548	4560	4572	4584	4596	4608	4620	4632	4644	4656	4668	4680	4692	4704	4716	4728	4740	4752	4764	4776	4788	4800	4812	4824	4836	4848	4860	4872	4884	4896	4908	4920	4932	4944	4956	4968	4980	4992	5004	5016	5028	5040	5052	5064	5076	5088	5100	5112	5124	5136	5148	5160	5172	5184	5196	5208	5220	5232	5244	5256	5268	5280	5292	5304	5316	5328	5340	5352	5364	5376	5388	5400	5412	5424	5436	5448	5460	5472	5484	5496	5508	5520	5532	5544	5556	5568	5580
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## ALIGNMENTS

RESULT 1
Q93R97
ID Q93R37 PRELIMINARY; PRT; 79 AA.
AC Q93R97;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RNA polymerase sigma factor (Fragment).
DN Name=rpoS;
GN Pseudomonas putida.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
[1]
RN SEQUENCE FROM N.A.
RP Ohmori D.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RA FUNCTION: Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released (By similarity).
CC CC -1- SIMILARITY: Belongs to the sigma-70 factor family.
DR ENBL; AB054812; BAB62001.1; -. HSP; Q9EZJ8; IKU3.
DR GG; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
DR GQ; GO:0016987; F:sigma factor activity; IEA.
DR GQ; GO:0003700; P:transcription factor activity; IEA.
DR GQ; GO:0016740; P:transferase activity; IEA.
DR GQ; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR GQ; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007630; Sigma70 r4.
DR Pfam; PF04545; Sigma70_r4; 1.
DR PRINTS; PR00046; SIGMA70FCT.
DR PROSITE; PS00716; SIGMA70_2; 1.
DR DNA-binding: DNA-directed RNA polymerase; Sigma factor; Transcription
KW Transcription regulation; Transferase.
NW NON_TER 1
FO SEQUENCE 79 AA: 91336 MW: AE74B2F1226CC213 CRC64;

Query Match	14.3%	Score 59	DB 2	Length 79;
Best Local Similarity	40.0%	Pred. No. 1.2e+02;		
Matches	22	Conservative 5	Mismatches 18	Indels 10
Gaps	2			
14	VRTGLRAE---	TEAVEVEIGRFDDQOYEMLKRWQQPAGLGA	VAAALRMGL	65
25	VRFGLRGHES	TTLEDVGLTGRTN-----	RVROIGVEGLKRLREILEKNGL	72

RESULT 2  
Q6TG30  
ID Q6TG30  
PRELIMINARY: PRT: 55 AA.

Q61G3V;  
AC 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

```
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Stationary phase sigma factor (Fragment).
GN Name=tpoS;
OS Azomonas macrocytogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azomonas.
OX NCBI_TaxID=69962;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12334;
RA Scott A., Meakins D., Page W.J.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Sigma factors are initiation factors that promote the
CC attachment of RNA polymerase to specific initiation sites and are
CC then released (by similarity).
CC -!- SIMILARITY: Belongs to the sigma-70 factor family.
DR EMBL; AY422193; AAS90415.1; -.
DR GO; GO:0016987; F:sigma factor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007630; Sigma70_r4.
DR InterPro; IPR000943; Sigma_70.
DR Pfam; PF04545; Sigma70_r4; 1.
DR PRINTS; PR00046; SIGMA70FCT.
DR PROSITE; PS00716; SIGMA70_2; 1.
DR DNA-binding; DNA-directed RNA polymerase; Sigma factor; Transcription;
KW Transcription regulation; Transference.
FT NON_TER 1
SQ SEQUENCE 55 AA; 6365 MW; 74760365FCB12854 CRC64;

Query Match 13.8%; Score 57; DB 2; Length 55;
Best Local Similarity 39.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 3; Mismatches 15; Indels 18; Gaps 3;

Qy 14 VRTGLGREAE---IEAVEVEIG-----RFRDQYEMLRWRQQPAGLGVVAALERMGL 65
Db 1 VRRFGLRHGESCTEEVEGQELGLTRVRQIQVEALKRLRE-----ILEKNGL 48

RESULT 3
Q7P321 PRELIMINARY; PRT; 59 AA.
AC Q7P321;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Virulence-associated protein 1.
GN Name=FN0340;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49256;
RA Katpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haselkorn R., Overbeek R., Kyrpides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABF0100154; EAA23321.1; -.
SQ SEQUENCE 59 AA; 6808 MW; 615C5DF19B318E86 CRC64;

Query Match 13.2%; Score 54.5; DB 2; Length 59;
Best Local Similarity 37.2%; Pred. No. 2.6e+02;
Matches 16; Conservative 5; Mismatches 21; Indels 1; Gaps 1;

Qy 11 KEFVRTGLGREAEIEA-VEVEIGRFRDQYEMLRWRQQPAG 52
Db 9 KGMVOLLGLPEKEITALINAEISISHDIMYRIVKTMHQKNYG 51
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RESULT 4
Q9ZXL9 PRELIMINARY; PRT; 69 AA.
AC Q9ZXL9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Pseudomonas aeruginosa phage phi CTX, complete genome sequence.
OS Bacteriophage phi CTX.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC P2-like viruses.
OX NCBI_TaxID=35343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=phiCTX-c;
RX MEDLINE=90014160; PubMed=2507866;
RA Hayashi T., Kamio Y., Hishinuma F., Usami Y., Titani K., Terawaki Y.;
RT "Pseudomonas aeruginosa cytotoxin: the nucleotide sequence of the gene
RT and the mechanism of activation of the protoxin.";
RL Mol. Microbiol. 3:861-868(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=phiCTX-c;
RX MEDLINE=99157549; PubMed=10027959;
RA Nakayama K., Kanaya S., Ohnishi M., Terawaki Y., Hayashi T.;
RT "The complete nucleotide sequence of phiCTX, a cytotoxin-converting
RT phage of Pseudomonas aeruginosa: implications for phage evolution and
RT horizontal gene transfer via bacteriophage.";
RL Mol. Microbiol. 31:399-419(1999).
DR EMBL; AB008550; BAA36234.1; -.
DR InterPro; IPR008861; Tail_X.
DR Pfam; PF05489; Phage_tail_X; 1.
SQ SEQUENCE 69 AA; 7436 MW; D2E35A698F195CC0 CRC64;

Query Match 13.1%; Score 54; DB 2; Length 69;
Best Local Similarity 45.8%; Pred. No. 3.5e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 3 DAVPARWKEFVRTGLGREAEIEA 26
Db 10 DTVEALCWRHYGRTAGVTAEVLEA 33

RESULT 5
Q6CZU0 PRELIMINARY; PRT; 78 AA.
AC Q6CZU0;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=EC4061;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Scri 1043 / ATCC BAA-672;
RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holvea M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bacon N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagers K., Moule S., Norbertczak H.,
RA Omond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmund G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG76958.1; -.
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DR InterPro; IPR008227; UCP006169.
DR InterPro; IPR010648; UFP0270.
DR Pfam; PF06794; UFP0270; 1.
DR PIRSF; PIRSF006169; UCP006169; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 78 AA; 8894 MW; CC29D8DC6F12BF9C CRC64;

Query Match 13.1%; Score 54; DB 2; Length 78;
Best Local Similarity 36.0%; Pred. No. 4e+02;
Matches 18; Conservative 4; Mismatches 16; Indels 12; Gaps 2;

Qy 41 MLKWRQOOPAGL-----GAVYAALERMGLDCGVEDLRSRLQRG 79
Db 1 MIIPQQLDPETLDSIIESFVLREGTDYGEQER-SLAQKVEDIRSLQSG 49

RESULT 6
Q8TYA5 PRELIMINARY; PRT; 79 AA.
AC Q8TYA5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Predicted RNA-binding protein containing the S4 domain.
GN OrderedLocusNames=MK0398;
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyzi; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RA MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
RX Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.I., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozlovskiy S.A.;
RP "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
DR EMBL; AE010336; AAM01613.1; -
DR GO; GO:0003723; rRNA binding; IEA.
DR Pfam; PF01479; S4; 1.
DR SMART; SM00363; S4; 1.
DR PROSITE; PS50889; S4; 1.
KW Complete proteome.
SQ SEQUENCE 79 AA; 8930 MW; 87B143AA16BAF7B5 CRC64;

Query Match 13.0%; Score 53.5; DB 2; Length 79;
Best Local Similarity 32.4%; Pred. No. 4.6e+02;
Matches 22; Conservative 7; Mismatches 26; Indels 13; Gaps 3;

Qy 8 RWKFEVFTLGLREAEIEAVE-VEIGRPDQOYEMLKWRQOOPAGLGVAVYAALERMGLD 66
Db 5 RLDDAFLKDVGLAESRRKRLVSGRVNGKLVKRPWLVSQ-----DEIEVD 55

Qy 67 GC---VED 71
Db 56 GVTVRVED 63

RESULT 7
Q72GH9 PRELIMINARY; PRT; 62 AA.
AC Q72GH9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TTIC1869;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
```

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OK NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15064768;
RA Henne A., Brueggemann H., Raasch C., Wierzer A., Hartach T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacob C., Starkuviene V., Schliep S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus.";
RL Nat. Biotechnol. 22:547-553 (2004).
DR EMBL; AE017307; AAS82211.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 62 AA; 7921 MW; 0D272F18D427D6EA CRC64;

Query Match 12.8%; Score 53; DB 2; Length 62;
Best Local Similarity 29.3%; Pred. No. 4e+02;
Matches 17; Conservative 14; Mismatches 25; Indels 2; Gaps 2;

Qy 8 RWKFEVFTLGLREAEIEA-VEVEIGRPDQOYEMLKWRQOOPAGLGVAVYAALERMG 64
Db 4 RRLKSVESYQARIREHQAKTEELRR-PEPRWELIRYWEKEIRTYPGRVERLLRRMG 60

RESULT 8
Q8U397 PRELIMINARY; PRT; 75 AA.
AC Q8U397;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PF0573.
GN OrderedLocusNames=PF0573;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VCI / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010180; AAL80697.1; -
DR Pfam; PF04014; SpoVT_AbrB; 1.
DR TIGRFAMs; TIGR01439; lp_hug_hel_AbrB; 1.
KW Complete proteome.
SQ SEQUENCE 75 AA; 8705 MW; 6FE2F4AF7D807146 CRC64;

Query Match 12.8%; Score 53; DB 2; Length 75;
Best Local Similarity 28.6%; Pred. No. 4.9e+02;
Matches 20; Conservative 14; Mismatches 24; Indels 12; Gaps 4;

Qy 5 VPARRWKEFVFTLGLREAEIEA-VEVEIGRPDQOYEMLKWRQOOPAG----LGAVYAAL 60
Db 14 IPA----EIRKALGIGKEGELLEVRLENGKI---IIRLUKRRKTKLKUGKUTLEIEIKAI 66

Qy 61 ERMGLDGCVE 70
Db 67 EE-GMKQCMQ 75

RESULT 9
Q7U9X2 PRELIMINARY; PRT; 78 AA.
AC Q7U9X2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=SYNW0130;
OS Synecococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
```



QY 17 LGLREABTEAIVEIGRFDQOYEMLKRWROQOPAGLGAIVAAALERMG 64  
DB 23 VGLRQGDKAIVEAINALHDSIQVYVK--NEIAQVGSISAADBEIG 67

## RESULT 13

ID Q93NF5 PRELIMINARY; PRT; 70 AA.  
AC Q93NF5;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE ORF70 (Hypothetical protein).  
OS Arthrobacter nicotinovorans.  
OS Plasmid pAO1, and Plasmid pAO1.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Micrococcineae; Micrococcaceae; Arthrobacter.  
OX NCBI\_TaxID=29320;  
RN [1]

SEQUENCE FROM N.A.  
RP PLASMID=pAO1, and pAO1;  
RC MEDLINE=21405725; PubMed=11514508;  
RX DOI=10.1128/JB.183.18.5262-5267.2001;  
RA Baitsch D., Sandu C., Brandsch R., Igloi G.L.;  
RT "Gene cluster on pAO1 of Arthrobacter nicotinovorans involved in  
RT degradation of the plant alkaloid nicotine: cloning, purification, and  
RT characterization of 2,6-dihydroxypyridine 3-hydroxylase.";  
RL J. Bacteriol. 183:5262-5267(2001).

## [2]

SEQUENCE FROM N.A.  
RP PLASMID=pAO1;  
RC MEDLINE=95115562; PubMed=7815950;  
RX Grether-Beck S., Igloi G.L., Fust S., Schiltz E., Decker K.,  
RA Brandsch R.;  
RT "Structural analysis and molybdenum-dependent expression of the pAO1-  
RT encoded nicotine dehydrogenase genes of Arthrobacter nicotinovorans.";  
RL Mol. Microbiol. 13:929-936(1994).

## [3]

SEQUENCE FROM N.A.  
RP PLASMID=pAO1;  
RC MEDLINE=96172783; PubMed=8588735;  
RX Menendez C., Igloi G., Henninger H., Brandsch R.;  
RT "A pAO1-encoded molybdopterin cofactor gene (moaA) of Arthrobacter  
RT nicotinovorans: characterization and site-directed mutagenesis of the  
RT encoded protein.";  
RL Arch. Microbiol. 164:142-151(1995).

## [4]

SEQUENCE FROM N.A.  
RP PLASMID=pAO1;  
RC MEDLINE=98088982; PubMed=9428706;  
RX Menendez C., Otto A., Igloi G., Nick P., Brandsch R., Schubach B.,  
RA Bottcher B., Brandsch R.;  
RT "Molybdate-uptake genes and molybdopterin-biosynthesis genes on a  
RT bacterial plasmid. Characterization of MoaA as a filament-forming  
RT protein with adenosinetriphosphatase activity.";  
RL Eur. J. Biochem. 250:524-531(1997).

## [5]

SEQUENCE FROM N.A.  
RP PLASMID=pAO1;  
RC MEDLINE=9906870; PubMed=9878353; DOI=10.1006/jmbi.1998.2227;  
RX Schenk S., Hoelz A., Kraus B., Decker K.;  
RT "Gene structure and properties of enzymes of the plasmid-encoded  
RT nicotine catabolism of Arthrobacter nicotinovorans.";  
RL J. Mol. Biol. 284:1323-1339(1998).

## [6]

SEQUENCE FROM N.A.  
RP PLASMID=pAO1;  
RC MEDLINE=97230479; PubMed=9073580; DOI=10.1006/plas.1996.1272;  
RX Menendez C., Igloi G.L., Brandsch R.;  
RT "IS1473, a putative insertion sequence identified in the plasmid pAO1  
RT from Arthrobacter nicotinovorans: isolation, characterisation and  
RT distribution among Arthrobacter species.";  
RL Plasmid 37:35-41(1997).

[7]  
RN SEQUENCE FROM N.A.  
RP PLASMID=pAO1;  
RX MEDLINE=22505657; PubMed=12618462;  
RX DOI=10.1128/JB.185.6.1976-1986.2003;  
RA Igloi G.L., Brandsch R.;  
RT "Sequence of the 16S-kilobase catabolic plasmid pAO1 from Arthrobacter  
RT nicotinovorans and identification of a pAO1-dependent nicotine uptake  
RT system.";  
RL J. Bacteriol. 185:1976-1986(2003).  
DR EMBL; AF373840; AAK64270.1; -;  
DR EMBL; AJ507836; CAD47929.1; -;  
KW Hypothetical protein; Plasmid.  
SQ SEQUENCE 70 AA; 7833 MW; 1501DDE147F444FF CRC64;

Query Match 12.6%; Score 52; DB 2; Length 70;

Best Local Similarity 36.6%; Pred. No. 5.8e+02;

Matches 15; Conservative 3; Mismatches 23; Indels 0; Gaps 0;

QY 35 RDQYEMLKRWROQOPAGLGAIVAAALERMGLDGCVEDLRSR 75  
DB 30 RDDQMTWLGRTDLPSPGLGCAADTKGRCCLCVNKSCHR 70

## RESULT 14

Q88AU2  
ID Q88AU2 PRELIMINARY; PRT; 66 AA.  
AC Q88AU2;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=PSPT00294;  
OS Pseudomonas syringae (pv. tomato).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=323;

## [1]

SEQUENCE FROM N.A.  
RP STRAIN=DC3000;  
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;  
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,  
RA Gwinn M.L., Dodson R.J., DeBoy R.F., Durkin A.S., Kolonay J.F.,  
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,  
RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,  
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,  
RA Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,  
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,  
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,  
RA Bender C.L., White O., Fraser C.M., Collier A.;  
RT "The complete genome sequence of the Arabidopsis and tomato pathogen  
RT Pseudomonas syringae pv. tomato DC3000.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).  
DR EMBL; AE016857; AA053839.1; -;  
DR TIGR; PSPT00294; -;  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 66 AA; 7274 MW; 6DD44F84FA4A630C CRC64;

Query Match 12.3%; Score 51; DB 2; Length 66;

Best Local Similarity 46.2%; Pred. No. 7e+02;

Matches 12; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 54 GAVYAAALERMGLDGCVEDLRSRLQRG 79  
DB 29 GAVATAFEKALDQMTADARRALQRG 54

## RESULT 15

Q7EYN4  
ID Q7EYN4 PRELIMINARY; PRT; 63 AA.  
AC Q7EYN4;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

```
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OSJNB0011E04.106.
GN Name=OSJNB0011E04.106;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005443; BAD05624.1; -.
KW Hypothetical protein.
SQ SEQUENCE 63 AA; 7063 MW; 348C125AE42F27D CRC64;

Query Match      12.2%; Score 50.5; DB 2; Length 63;
Best Local Similarity 32.8%; Pred. No. 7.6e+02;
Matches 21; Conservative 8; Mismatches 20; Indels 15; Gaps 4;

Qy 4 AVPARRWKEFVRTGLREAETEAV-----EVEIGFRDQOYEMLKRWQQQPAGLGAVYA 58
Db 10 ACGGRRWRPPRWEGRR--RIGAVSFPPPDLAVGR---AQWEGSRRW-----PGVPATVA 59

Qy 59 ALER 62
Db 60 AVRR 63
```

Search completed: June 27, 2005, 14:40:56  
Job time : 174 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:22:33 ; Search time 158 Seconds  
(without alignments)  
195.828 Million cell updates/sec

Title: US-10-081-280-6\_COPY\_338\_417

Perfect score: 413  
Sequence: 1 VMDAVPARWKEFVRTTLGLR.....ERMGLDGCVEDLRSLRQGP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1092469

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	381	92.3	74	5	ABG31492 Human Apo
2	381	92.3	74	7	ADG98744 Apo-3/DR3
3	381	92.3	74	8	ADO40453 Human Apo
4	338	81.8	65	2	AAW93610 Human DR3
5	338	81.8	65	3	AAW93610 Human DR3
6	155	37.5	78	5	ABG31493 Human Apo
7	155	37.5	78	6	ADA49709 Death dom
8	155	37.5	78	7	ADG98745 TNFR1 dea
9	155	37.5	78	8	ADO40454 Human TNF
10	142	34.4	69	2	AAW93612 Human TNF
11	139	33.7	30	4	AAO08695 Human Pol
12	136.5	33.1	68	3	AB26989 Human TNF
13	118	28.6	64	2	AAW00208 Human p55
14	105	25.4	75	7	ADG42594 NOV1 doma
15	94	22.8	76	8	ADO40451 Human Apo
16	83	20.1	67	3	AB26992 Human DR5
17	82	19.9	67	2	AAW93613 Human CAR
18	77.5	18.8	67	3	AAV67948 Tumour ne
19	74	17.9	45	4	AAW89832 Human imm
20	74	17.9	76	7	ADG98743 DR4 death
21	74	17.9	76	8	ADO40452 Human DR4
22	70.5	17.1	77	6	ADA49713 Death dom
23	68	16.5	67	3	AB26991 Human DR4
24	67	16.2	51	2	AB99285 Partial h
25	64.5	15.6	65	5	AAE24868 Chlamydia

26	64.5	15.6	65	5	AAE38911	Aae38911 Chlamydia
27	60	14.5	77	2	AAW62177	Aaw62177 Nerve gro
28	60	14.5	77	8	ADJ25858	Adj25858 Nerve gro
29	57.5	13.9	63	2	AAW00206	Aaw00206 Human Fas
30	57.5	13.9	68	2	AAW93611	Aaw93611 Human Fas
31	57.5	13.9	68	3	AB26988	Ab26988 Human CD9
32	57.5	13.9	68	4	AAW80357	Aaw80357 Human hae
33	57.5	13.9	77	5	ABG31494	Abg31494 Human Apo
34	57.5	13.9	77	6	ADA49710	Ada49710 Death dom
35	57.5	13.9	77	7	ADG98746	Adg98746 Fas/Apo1
36	57.5	13.9	77	8	ADO40455	Ado40455 Human Fas
37	57	13.8	65	5	AAE24866	Aae24866 Chlamydia
38	57	13.8	65	5	AAE38909	Aae38909 Chlamydia
39	57	13.8	71	5	AAE24857	Aae24857 Mouse NGF
40	57	13.8	71	5	AAE38900	Aae38900 Mouse NGF
41	56.5	13.7	73	8	ADN46273	Adn46273 Thermococ
42	56	13.6	65	5	AAE24856	Aae24856 Chlamydia
43	56	13.6	65	5	AAE38899	Aae38899 Chlamydia
44	55	13.3	60	4	AAU63529	Aau63529 Propionib
45	55	13.3	60	6	ABM60048	Abm60048 Propionib

ALIGNMENTS

RESULT 1  
ABG31492  
ID ABG31492 standard; protein; 74 AA.  
XX  
AC ABG31492;  
XX  
DT 21-NOV-2002 (first entry)  
XX  
DE Human Apo-2DcR associated protein #2.  
XX  
KW Human; Apo-2DcR; Apo-2 ligand; programmed cell death; apoptosis;  
KW neurodegenerative disease; autoimmune; inflammatory.  
XX  
OS Homo sapiens.  
XX  
PN US2002102706-A1.  
XX  
PD 01-AUG-2002.  
XX  
PF 21-JUN-2001; 2001US-00887879.  
XX  
PR 18-JUN-1997; 97US-0049911P.  
PR 12-JUN-1998; 98US-00096500.  
XX  
(GETH ) GENENTECH INC.  
XX  
Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A, Kim KJ;  
Wood WI;  
XX  
WPI; 2002-697823/75.  
XX  
Novel isolated Apo-2DcR polypeptide useful for modulating apoptosis in  
mammalian cells.  
XX  
Disclosure; Page 37; 58pp; English.

The present invention relates to the isolation of novel human polypeptides, designated Apo-2DcR, and the polynucleotide sequences encoding them. Apo-2DcR is capable of binding Apo-2 ligand and is useful for modulating programmed cell death or apoptosis in mammalian cells. Apo-2DcR can be used to produce apo-2DcR antibodies which are useful therapeutically, and can cross-react with other receptors for Apo-2 ligand to block excessive apoptosis in neurodegenerative diseases, or to block potentially autoimmune or inflammatory effects. Apo-2DcR antibodies are also useful in immunohistochemistry staining assays or diagnostic assays for Apo-2DcR, e.g. detecting it's expression in specific cells, tissues or serum, and for the affinity purification of Apo-2DcR from recombinant cell culture or natural sources. The present sequence



CC represents a protein of unknown function relating to the present  
CC invention. Note: The present sequence is given in the Seq listing but is  
CC not mentioned elsewhere in the specification  
XX  
SQ Sequence 74 AA;

Query Match 92.3%; Score 381; DB 5; Length 74;  
Best Local Similarity 100.0%; Pred. No. 5e-41;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMDAVPARRWKEFVRTGLREAEIAEVEIGRFRDQOQYEMLKRWRQQPAGLGAVYAAL 60  
Dy 1 VMDAVPARRWKEFVRTGLREAEIAEVEIGRFRDQOQYEMLKRWRQQPAGLGAVYAAL 60

Qy 61 ERMGLDGCVEDLRS 74  
Dy 61 ERMGLDGCVEDLRS 74

RESULT 2  
ADG98744  
ID ADG98744 standard; protein; 74 AA.  
XX AC ADG98744;  
XX DT 11-MAR-2004 (first entry)  
XX DE Apo-3/DR3 death domain protein.  
XX KW Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;  
XX KW cancer; gene therapy.  
XX OS Unidentified.  
XX FN US2003148455-A1.  
XX PD 07-AUG-2003.  
XX PF 06-NOV-2002; 2002US-00288917.  
XX 15-MAY-1997; 97US-0046615P.  
PR 09-FEB-1998; 98US-0074119P.  
PR 14-MAY-1998; 98US-00079029.  
PR 02-NOV-2001; 2001US-00052798.  
XX PA (GETH ) GENENTECH INC.  
XX PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
XX WPI; 2003-897574/82.  
XX PT New Apo-2 polypeptide or its extracellular or death domain sequence,  
PT useful for modulating apoptosis in mammalian cancer cells or for  
PT generating transgenic or knockout animals.  
XX PS Disclosure; Fig 2B; 64pp; English.  
XX CC The present invention provides novel Apo-2 protein and the nucleic acid  
CC encoding the protein. The invention is useful in inducing apoptosis in  
CC mammalian cancer cells. The invention is also useful in diagnostic  
CC procedures for tissue-specific typing and in generating transgenic  
CC animals that are useful in development and screening of reagents. The  
CC invention is also useful in gene therapy. The present sequence is  
CC Apo3/DR3 death domain protein.  
XX  
SQ Sequence 74 AA;

Query Match 92.3%; Score 381; DB 7; Length 74;  
Best Local Similarity 100.0%; Pred. No. 5e-41;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMDAVPARRWKEFVRTGLREAEIAEVEIGRFRDQOQYEMLKRWRQQPAGLGAVYAAL 60  
Dy 1 VMDAVPARRWKEFVRTGLREAEIAEVEIGRFRDQOQYEMLKRWRQQPAGLGAVYAAL 60

Db 1 VMDAVPARRWKEFVRTGLREAEIAEVEIGRFRDQOQYEMLKRWRQQPAGLGAVYAAL 60  
Qy 61 ERMGLDGCVEDLRS 74  
Dy 61 ERMGLDGCVEDLRS 74

RESULT 3  
ADO40453  
ID ADO40453 standard; protein; 74 AA.  
XX AC ADO40453;  
XX DT 15-JUL-2004 (first entry)  
XX DE Human Apo-3/DR3 protein.  
XX KW Apo-2 protein; apoptosis; cancer; tissue typing; transgenic animal;  
XX KW gene therapy; human; Apo-3/DR3.  
XX OS Homo sapiens.  
XX FN US2004009552-A1.  
XX PD 15-JAN-2004.  
XX PF 25-APR-2003; 2003US-00423448.  
XX 15-MAY-1997; 97US-0046615P.  
PR 09-FEB-1998; 98US-0074119P.  
PR 14-MAY-1998; 98US-00079029.  
PR 02-NOV-2001; 2001US-00052798.  
PR 06-NOV-2002; 2002US-00288917.  
XX PA (GETH ) GENENTECH INC.  
XX PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
XX WPI; 2004-090468/09.  
XX PT New Apo-2 polypeptides and encoding nucleic acid molecules, useful for  
PT diagnosing, preventing or treating cancer, and in tissue typing or in  
PT generating antibodies or transgenic animals.  
XX PS Example 1; Fig 2B; 53pp; English.  
XX CC The present invention provides novel Apo-2 polypeptide and the encoding  
CC polynucleotide capable of modulating apoptosis. The invention is useful  
CC in diagnosing, treating and preventing cancer, tissue typing, in  
CC generating antibodies and transgenic animals. The invention is also  
CC useful in gene therapy. The present sequence is human Apo-3/DR3 protein.  
CC This sequence is used in the exemplification of the invention  
XX  
SQ Sequence 74 AA;

Query Match 92.3%; Score 381; DB 8; Length 74;  
Best Local Similarity 100.0%; Pred. No. 5e-41;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMDAVPARRWKEFVRTGLREAEIAEVEIGRFRDQOQYEMLKRWRQQPAGLGAVYAAL 60  
Dy 1 VMDAVPARRWKEFVRTGLREAEIAEVEIGRFRDQOQYEMLKRWRQQPAGLGAVYAAL 60

Qy 61 ERMGLDGCVEDLRS 74  
Dy 61 ERMGLDGCVEDLRS 74

RESULT 4  
AAW93610  
ID AAW93610 standard; protein; 65 AA.  
XX AC AAW93610;

XX 18-JUN-1999 (first entry)  
XX Human DR3 protein fragment.  
XX Killer protein; adriamycin inducible; human; chromosome 8p21; diagnosis;  
KW p53-inducible; apoptosis-mediating activity; treatment; animal model;  
KW neoplastic disease; DR3.  
XX  
XX Homo sapiens.  
XX WO9502653-A1.  
XX  
XX 21-JAN-1999.  
XX  
XX 10-JUL-1998; 98WO-US014495.  
XX  
XX 11-JUL-1997; 97US-0052305P.  
PR 04-AUG-1997; 97US-0054710P.  
PR 30-SEP-1997; 97US-0060473P.  
PR 11-MAR-1998; 98US-0077526P.  
PR 11-MAR-1998; 98US-0077628P.  
PR 11-MAR-1998; 98US-0077661P.  
XX  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX  
XX El-Deiry WS;  
XX  
XX WPI; 1999-120857/10.  
XX  
XX A new nucleic acid encodes a p53-induced protein (Killer) - which induces  
PT apoptosis and is useful in the diagnosis and treatment of neoplastic  
PT diseases.  
XX  
XX Disclosure; Page 46; 65pp; English.  
XX This invention describes a novel human adriamycin-inducible killer  
CC protein located on chromosome 8p21, which also has p53-inducible,  
CC apoptosis-mediating activity and comprises an amino-terminal  
CC extracellular receptor, transmembrane and death domains. The nucleic acid  
CC molecule which encodes the protein, it's encoded signal transduction  
CC protein and antibodies of the invention are useful in the diagnosis and  
CC treatment of neoplastic diseases. The invention is also useful for the  
CC production of animal model systems  
XX  
XX Sequence 65 AA;  
Query Match 81.8%; Score 338; DB 2; Length 65;  
Best Local Similarity 100.0%; Pred. No. 1.5e-35;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 RWKEFVRLGLREAEIEAVEVEIGRFRDQYEMLKRWQQQPAGLGAVYAALERMGLDGC 68  
Db 1 RWKEFVRLGLREAEIEAVEVEIGRFRDQYEMLKRWQQQPAGLGAVYAALERMGLDGC 60  
QY 69 VEDLR 73  
Db 61 VEDLR 65  
RESULT 5  
AAB26990  
ID AAB26990 standard; protein; 65 AA.  
XX  
XX AAB26990;  
XX  
XX 02-FEB-2001 (first entry)  
XX Human DR3 death domain.  
XX Human; tumour necrosis factor; TNF; TR9 receptor; immunosuppressive;  
KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;  
KW antiathritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;  
XX

KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;  
KW common variable immunodeficiency; X-linked agammaglobulinaemia;  
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;  
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;  
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;  
KW cardiovascular disease; neurological disease; protein coordinate data;  
XX osteoprotegerin; DR3.  
XX Homo sapiens.  
XX WO200056862-A1.  
XX  
XX 28-SEP-2000.  
XX  
XX 16-MAR-2000; 2000WO-US006831.  
XX  
XX 24-MAR-1999; 99US-0126019P.  
PR 14-MAY-1999; 99US-0134220P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ni J, Gentz RL, Yu G, Fan P;  
XX WPI; 2000-594575/56.  
XX  
XX Nucleic acid molecule encoding a human tumor necrosis factor receptor,  
PT known as TR9, useful for treating, preventing and diagnosing severe  
PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy  
PT and cancer.  
XX  
XX Disclosure; Fig 4C; 220pp; English.  
XX The present sequence is the death domain of DR3. It was used for  
CC comparison to a domain of a novel human tumour necrosis factor receptor,  
CC designated TR9. The TR9 receptor is also known as Death Domain Containing  
CC Receptor 5. TR9 polypeptides, polynucleotides or agonists are useful for  
CC treating, preventing or diagnosing common variable immunodeficiency, X-  
CC linked agammaglobulinaemia, severe combined immunodeficiency and Wiskott-  
CC Aldrich syndrome, autoimmune diseases (such as rheumatoid arthritis,  
CC allergic encephalomyelitis, multiple sclerosis, diabetes mellitus and  
CC asthma), HIV infection, epilepsy, cancer, cardiovascular diseases and  
CC other neurological diseases  
XX  
XX Sequence 65 AA;  
Query Match 81.8%; Score 338; DB 3; Length 65;  
Best Local Similarity 100.0%; Pred. No. 1.5e-35;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 RWKEFVRLGLREAEIEAVEVEIGRFRDQYEMLKRWQQQPAGLGAVYAALERMGLDGC 68  
Db 1 RWKEFVRLGLREAEIEAVEVEIGRFRDQYEMLKRWQQQPAGLGAVYAALERMGLDGC 60  
QY 69 VEDLR 73  
Db 61 VEDLR 65  
RESULT 6  
ABG31493  
ID ABG31493 standard; protein; 78 AA.  
XX  
XX ABG31493;  
XX  
XX 21-NOV-2002 (first entry)  
XX Human Apo-2DcR associated protein #3.  
XX Human; Apo-2DcR; Apo-2 ligand; programmed cell death; apoptosis;  
KW neurodegenerative disease; autoimmune; inflammatory.  
XX Homo sapiens.  
XX

PN US2002102706-A1.  
XX 01-AUG-2002.  
PD 21-JUN-2001; 2001US-00887879.  
XX 18-JUN-1997; 97US-0049911P.  
PR 12-JUN-1998; 98US-00096500.  
XX (GETH ) GENENTECH INC.  
PA Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A, Kim KJ;  
PI Wood WJ;  
XX WPI; 2002-697823/75.  
XX Novel isolated Apo-2DcR polypeptide useful for modulating apoptosis in  
PT mammalian cells.  
XX Disclosure; Page 37; 58pp; English.  
XX The present invention relates to the isolation of novel human  
CC polypeptides, designated Apo-2DcR, and the polynucleotide sequences  
CC encoding them. Apo-2DcR is capable of binding Apo-2 ligand and is useful  
CC for modulating programmed cell death or apoptosis in mammalian cells. Apo  
CC -2DcR can be used to produce apo-2DcR antibodies which are useful  
CC therapeutically, and can cross-react with other receptors for Apo-2  
CC ligand to block excessive apoptosis in neurodegenerative diseases, or to  
CC block potentially autoimmune or inflammatory effects. Apo-2DcR antibodies  
CC are also useful in immunohistochemistry staining assays or diagnostic  
CC assays for Apo-2DcR, e.g. detecting it's expression in specific cells,  
CC tissues or serum, and for the affinity purification of Apo-2DcR from  
CC recombinant cell culture or natural sources. The present sequence  
CC represents a protein of unknown function relating to the present  
CC invention. Note: The present sequence is given in the Seq listing but is  
CC not mentioned elsewhere in the specification  
XX  
SQ Sequence 78 AA;  
Query Match 37.5%; Score 155; DB 5; Length 78;  
Best Local Similarity 46.1%; Pred. No. 7e-12; Indels 4; Gaps 2;  
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;  
QY 1 VMDAVPARRWKEFVRTLGLEAEAEVEVEIGR-FRDQQYEMLKRWQQQP---AGLGAV 56  
Db 1 VVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQYSMLATWRRTPRREATLELL 60  
QY 57 YAALERMGLDGCVEDL 72  
Db 61 GRVLRDMDLLGCLEDI 76  
RESULT 7  
ADA49709  
ID ADA49709 standard; protein; 78 AA.  
XX ADA49709;  
AC ADA49709;  
XX 20-NOV-2003 (first entry)  
DT Death domain of human TNFR1 (htnfr1) protein.  
DE Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity;  
XX competitive-type receptor; binding assay; cancer cell; human;  
KW TNF receptor family; htnfr1; death domain; cytostatic.  
XX Homo sapiens.  
OS US2002192729-A1.  
XX 19-DEC-2002.  
PD 28-MAR-2002; 2002US-00112793.  
PF

XX 01-APR-1996; 96US-00625328.  
PR 23-SEP-1996; 96US-00710802.  
PR 31-MAR-1997; 97US-00828683.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ;  
PI WPI; 2003-657226/62.  
XX Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or  
PT Apo-3 polypeptide which induces or stimulates apoptotic activity, useful  
PT in diagnostic assays.  
XX Disclosure; Fig 6; 53pp; English.  
XX The present invention relates to the isolation of a biologically active  
CC Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide  
CC sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The  
CC Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI  
CC is useful for generating antibodies, as standards in assays for Apo-3 or  
CC Apo-2LI, in affinity purification techniques, and in competitive-type  
CC receptor binding assays when labelled with radioiodine, enzymes or  
CC fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or  
CC inducing apoptosis in cancer cells, and thus have therapeutic utility.  
CC The present sequence represents the death domain of a human TNF receptor  
CC family protein. This sequence is compared with the death domain of human  
CC Apo-3.  
XX  
SQ Sequence 78 AA;  
Query Match 37.5%; Score 155; DB 6; Length 78;  
Best Local Similarity 46.1%; Pred. No. 7e-12; Indels 4; Gaps 2;  
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;  
QY 1 VMDAVPARRWKEFVRTLGLEAEAEVEVEIGR-FRDQQYEMLKRWQQQP---AGLGAV 56  
Db 1 VVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQYSMLATWRRTPRREATLELL 60  
QY 57 YAALERMGLDGCVEDL 72  
Db 61 GRVLRDMDLLGCLEDI 76  
RESULT 8  
ADG98745  
ID ADG98745 standard; protein; 78 AA.  
XX ADG98745;  
AC ADG98745;  
XX 11-MAR-2004 (first entry)  
DT TNFR1 death domain protein.  
DE Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;  
XX cancer; gene therapy.  
XX Unidentified.  
OS US2003148455-A1.  
XX 07-AUG-2003.  
PD 06-NOV-2002; 2002US-00288917.  
PF 15-MAY-1997; 97US-0046615P.  
XX 09-FEB-1998; 98US-0074119P.  
PR 14-MAY-1998; 98US-00079029.  
PR 02-NOV-2001; 2001US-00052798.  
XX (GETH ) GENENTECH INC.  
XX

PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
XX WPI; 2003-897574/82.  
XX New Apo-2 polypeptide or its extracellular or death domain sequence,  
XX useful for modulating apoptosis in mammalian cancer cells or for  
XX generating transgenic or knockout animals.  
XX Disclosure; Fig 2B; 64pp; English.  
XX The present invention provides novel Apo-2 protein and the nucleic acid  
XX encoding the protein. The invention is useful in inducing apoptosis in  
XX mammalian cancer cells. The invention is also useful in diagnostic  
XX procedures for tissue-specific typing and in generating transgenic  
XX animals that are useful in development and screening of reagents. The  
XX invention is also useful in gene therapy. The present sequence is TNFR1  
XX (tumour necrosis factor receptor 1) death domain protein.  
XX Sequence 78 AA;  
SQ

Query Match 37.5%; Score 155; DB 7; Length 78;  
Best Local Similarity 46.1%; Pred. No. 7e-12;  
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;  
QY 1 VMDAVPARRWKEFVRTGLREABIEAVEVEIGR-FRQOQYEMLKRWQQQP---AGLCGV 56  
Db 1 VVENVPPLRWKEFVRLGLSDHEIDRLQNGRCLREAQYSLATWRRTPRREATLELL 60  
QY 57 YAALERMGDGCVEDL 72  
Db 61 GRVLRLDMLLGCLEDI 76

RESULT 9  
ADO40454  
ID ADO40454 standard; protein; 78 AA.  
XX ADO40454;  
XX 15-JUL-2004 (first entry)  
XX Human TNFR1 protein.  
XX Apo-2 protein; apoptosis; cancer; tissue typing; transgenic animal;  
XX gene therapy; human; TNFR1; receptor.  
XX Homo sapiens.  
XX US2004009552-A1.  
XX 15-JAN-2004.  
XX 25-APR-2003; 2003US-00423448.  
XX 15-MAY-1997; 97US-0046615P.  
XX 09-FEB-1998; 98US-0074119P.  
XX 14-MAY-1998; 98US-00079029.  
XX 02-NOV-2001; 2001US-00052798.  
XX 06-NOV-2002; 2002US-00288917.  
XX (GETH ) GENENTECH INC.  
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
XX WPI; 2004-090468/09.  
XX New Apo-2 polypeptides and encoding nucleic acid molecules, useful for  
XX diagnosing, preventing or treating cancer, and in tissue typing or in  
XX generating antibodies or transgenic animals.  
XX Example 1; Fig 2B; 53pp; English.  
XX The present invention provides novel Apo-2 polypeptide and the encoding

CC polynucleotide capable of modulating apoptosis. The invention is useful  
CC in diagnosing, treating and preventing cancer, tissue typing, in  
CC generating antibodies and transgenic animals. The invention is also  
CC useful in gene therapy. The present sequence is human TNFR1 protein. This  
CC sequence is used in the exemplification of the invention  
XX Sequence 78 AA;  
SQ

Query Match 37.5%; Score 155; DB 8; Length 78;  
Best Local Similarity 46.1%; Pred. No. 7e-12;  
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;  
QY 1 VMDAVPARRWKEFVRTGLREABIEAVEVEIGR-FRQOQYEMLKRWQQQP---AGLCGV 56  
Db 1 VVENVPPLRWKEFVRLGLSDHEIDRLQNGRCLREAQYSLATWRRTPRREATLELL 60  
QY 57 YAALERMGDGCVEDL 72  
Db 61 GRVLRLDMLLGCLEDI 76

RESULT 10  
AAW93612  
ID AAW93612 standard; protein; 69 AA.  
XX AAW93612;  
XX 18-JUN-1999 (first entry)  
XX Human TNFR-1 protein fragment.  
XX Killer protein; adriamycin inducible; human; chromosome 8p21; diagnosis;  
XX p53-inducible; apoptosis-mediating activity; treatment; animal model;  
XX neoplastic disease; TNFR-1.  
XX Homo sapiens.  
XX WO9902653-A1.  
XX 21-JAN-1999.  
XX 10-JUL-1998; 98WO-US014495.  
XX 11-JUL-1997; 97US-0052305P.  
XX 04-AUG-1997; 97US-0054710P.  
XX 30-SEP-1997; 97US-0060473P.  
XX 11-MAR-1998; 98US-0077526P.  
XX 11-MAR-1998; 98US-0077628P.  
XX 11-MAR-1998; 98US-0077661P.  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX EL-Deiry WS;  
XX WPI; 1999-120857/10.  
XX A new nucleic acid encodes a p53-induced protein (Killer) - which induces  
XX apoptosis and is useful in the diagnosis and treatment of neoplastic  
XX diseases.  
XX Disclosure; Page 46; 65pp; English.  
XX This invention describes a novel human adriamycin-inducible killer  
XX protein located on chromosome 8p21, which also has p53-inducible,  
XX apoptosis-mediating activity and comprises an amino-terminal  
XX extracellular receptor, transmembrane and death domains. The nucleic acid  
XX molecule which encodes the protein, it's encoded signal transduction  
XX protein and antibodies of the invention are useful in the diagnosis and  
XX treatment of neoplastic diseases. The invention is also useful for the  
XX production of animal model systems  
XX Sequence 69 AA;  
SQ



```
RESULT 13
AAW00208
ID AAW00208 standard; peptide; 64 AA.
XX
XX
AC AAW00208;
XX
DT 16-APR-1997 (first entry)
XX
DE Human p55 tumour necrosis factor receptor death domain motif.
XX
KW Death domain; regulatory protein; NGF-R; nerve growth receptor; FAS-R;
KW Fas ligand receptor; Fas/ABO1; ankyrin 1; p55 TNF-R;
KW tumour necrosis factor receptor; MORT1; cell cytotoxicity; HIV;
KW human immunodeficiency virus; cancer; neoplasia; disease.
XX
XX Homo sapiens.
XX
XX WO9625941-A1.
XX
PD 29-AUG-1996.
XX
PF 15-FEB-1996; 96WO-US002326.
XX
PR 22-FEB-1995; 95IL-00112742.
PR 13-SEP-1995; 95IL-00115289.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX PA (WEIN/) WEINWURZEL H.
XX
XX Wallach D, Boldin MP, Varfolomeev EE, Pancer Z, Mett I;
XX PI Goncharov TM;
XX
XX WPI; 1996-402125/40.
XX
PT Modulator of regulatory cellular events mediated by "death domain" contg.
PT regulatory proteins - useful for modulating functions mediated in cells
PT by proteins contg the death domain.
XX
XX Claim 9; Fig 1; 74pp; English.
XX
XX AAW00207 shows the death domain of the p55 tumour necrosis factor
XX receptor (p55 TNF-R). The death domain (DD) of human Fas-ligand receptor
XX (FAS-R), ankyrin 1, nerve growth factor receptor (NGF-R) and MORT-1
XX (which binds to the intracellular portion of (FAS-R)) are also given (see
XX AAW00206-07 and AAW00209-W00210). These DDs are used to identify
XX compounds capable of modulating activity of the regulatory proteins (p55,
XX NGF, TNF and FAS-R ligand, MORT-1) via interaction with the DDs. Such
XX modulators which may be antibodies, antisense sequences or ribozymes
XX (which can affect the cellular mRNA sequences encoding the proteins) and
XX are useful for modulation of effects of the regulatory proteins within
XX the cell. Tumour cells, HIV-infected cells or other diseased cells can be
XX treated by targeting the cells with animal viral vectors encoding the
XX modulators and a viral surface antigen capable of binding to a specific
XX receptor. The DDs are characterised by having groups of common amino acid
XX residues Trp, Ala, Asp, Glu, Thr, Arg and Tyr within locations that can
XX be aligned to show homology
XX
XX Sequence 64 AA;
XX
XX Query Match 28.6%; Score 118; DB 2; Length 64;
XX Best Local Similarity 42.6%; Pred. NO. 3.2e-07;
XX Matches 29; Conservative 10; Mismatches 17; Indels 12; Gaps 3;
XX
XX QY 10 WKFEVRLGLRAEAEVEIGR-FRDOQYEMLRKRWQOOPAGIGAVYAALERMG-----64
XX DB 1 WKFEVRLGLSDHEIDRLQLONGRCLEAQISMLATWRRTRPR-----EATLELGRVLR 56
XX
XX QY 65 ---LDGCV 69
XX DB 57 DHDLLGLCL 64
```

```
RESULT 14
ADG42594
ID ADG42594 standard; protein; 75 AA.
XX
XX AC ADG42594;
XX
XX 26-FEB-2004 (first entry)
XX
XX NOV1 domain analysis associated protein seq id 47.
XX
XX cytosstatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
XX NOVX-associated disorder; cancer; NOVX; domain analysis.
XX
XX Unidentified.
XX
XX US2003204052-A1.
XX
XX 30-OCT-2003.
XX
XX 04-OCT-2001; 2001US-00970944.
XX
XX 04-OCT-2000; 2000US-0237862P.
XX
XX (HERR/) HERRMANN J L.
XX PA (RAST/) RASTELLI L.
XX PA (SHIM/) SHIMKETS R A.
XX
XX Herrmann JL, Rastelli L, Shimkets RA;
XX
XX WPI; 2003-900673/82.
XX
XX New NOVX gene or NOVX-specific antibody, useful for preparing a
XX composition for treating or preventing a NOVX-associated disorder, e.g.,
XX cancer.
XX
XX Disclosure; SEQ ID NO 47; 118pp; English.
XX
XX The invention describes a new isolated polypeptide comprising: a
XX polypeptide or its mature form comprising a sequence not given in the
XX specification; or a variant of (A), where one or more amino acid residues
XX in the variant differs in no more than 15% from the amino acid sequence
XX of the mature form. The pharmaceutical composition may be administered
XX via oral, transdermal, rectal or parenteral route. The polypeptide,
XX nucleic acid or antibody is useful for preparing a composition for
XX treating or preventing a NOVX-associated disorder, e.g., cancer. This is
XX the amino acid sequence of a protein associated with analysis of domains
XX in human NOV1 protein.
XX
XX Sequence 75 AA;
XX
XX Query Match 25.4%; Score 105; DB 7; Length 75;
XX Best Local Similarity 35.3%; Pred. No. 1.8e-05;
XX Matches 24; Conservative 12; Mismatches 30; Indels 2; Gaps 1;
XX
XX QY 1 VMDAVPARRWKEFVRTGLRRAEAEVEIGRFRDOQYEMLRKRWQO--OPAGIGAVYA 58
XX DB 6 LLDDPLGRDWRRLARKLGSEEDIQIEHENPRLASPTYQLLDIWEQRGKGNATVTGLE 65
XX
XX QY 59 ALERMGD 66
XX DB 66 ALRKGGRD 73
XX
XX RESULT 15
ADO40451
ID ADO40451 standard; protein; 76 AA.
XX
XX AC ADO40451;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human Apo-2 protein #2.
XX
```

KW Apo-2 protein; apoptosis; cancer; tissue typing; transgenic animal;  
KW gene therapy; human.  
XX  
OS Homo sapiens.  
XX  
FN US2004009552-A1.  
XX  
XX  
PD 15-JAN-2004.  
XX  
XX  
PF 25-APR-2003; 2003US-00423448.  
XX  
XX 15-MAY-1997; 97US-0046615P.  
PR 09-FEB-1998; 98US-0074119P.  
PR 14-MAY-1998; 98US-00079029.  
PR 02-NOV-2001; 2001US-00052798.  
PR 06-NOV-2002; 2002US-00288917.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
XX  
XX WPI; 2004-090468/09.  
DR  
XX  
XX New Apo-2 polypeptides and encoding nucleic acid molecules, useful for  
PT diagnosing, preventing or treating cancer, and in tissue typing or in  
PT generating antibodies or transgenic animals.  
XX  
XX Example 1; SEQ ID NO 14; 53pp; English.  
XX  
XX The present invention provides novel Apo-2 polypeptide and the encoding  
CC polynucleotide capable of modulating apoptosis. The invention is useful  
CC in diagnosing, treating and preventing cancer, tissue typing, in  
CC generating antibodies and transgenic animals. The invention is also  
CC useful in gene therapy. The present sequence is human Apo-2 protein. This  
CC sequence is used in the exemplification of the invention  
XX  
SQ Sequence 76 AA;  
  
Query Match 22.8%; Score 94; DB 8; Length 76;  
Best Local Similarity 34.4%; Pred. No. 0.00049;  
Matches 22; Conservative 11; Mismatches 29; Indels 2; Gaps 1;  
  
Qy 3 DAVPARRWKFEVRTLGLREAEIEAVEVEIGRFRDQOYEMLKRW--RQQQPAGLGAVYAAL 60  
| | | | | : | | | | | : | | | | | : | | : | |  
Db 3 DLVFPDSWEPLMRKLGMLMDNEIKVAKAEAGHRDTLYTMLIKWVNTKGRDASVHTLLDAL 62  
| | | | | : | | | | | : | | | | | : | | : | |  
  
Qy 61 ERMG 64  
| | |  
Db 63 ETLG 66  
| | |  
  
Search completed: June 27, 2005, 14:37:58  
Job time : 160 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:38:10 ; Search time 163 Seconds  
(without alignments)  
188.735 Million cell updates/sec

Title: US-10-081-280-6\_COPY\_338\_417

Perfect score: 413

Sequence: 1 VMDAVPARRWKEFVRTIGLR.....ERMGLDGCVDLRRLRQGP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 666033

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/FCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
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12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	381	92.3	74	9	US-09-887-879-15
2	381	92.3	74	9	US-09-992-964-15
3	381	92.3	74	14	US-10-207-295-9
4	381	92.3	74	14	US-10-242-383-15
5	338	81.8	65	9	US-09-756-854-24
6	338	81.8	65	13	US-10-041-574-24
7	338	81.8	65	16	US-10-834-966-24
8	155	37.5	78	9	US-09-887-879-16
9	155	37.5	78	9	US-09-992-964-15
10	155	37.5	78	13	US-10-112-793-23
11	155	37.5	78	14	US-10-207-295-10
Sequence 15, Appl					
Sequence 15, Appl					
Sequence 9, Appl					
Sequence 15, Appl					
Sequence 24, Appl					
Sequence 24, Appl					
Sequence 16, Appl					
Sequence 16, Appl					
Sequence 23, Appl					

12	155	37.5	78	14	US-10-242-383-16	Sequence 16, Appl
13	136.5	33.1	68	9	US-09-756-854-23	Sequence 23, Appl
14	136.5	33.1	68	13	US-10-041-574-23	Sequence 23, Appl
15	136.5	33.1	68	16	US-10-834-966-23	Sequence 23, Appl
16	118	28.6	64	13	US-10-035-408-3	Sequence 3, Appl
17	94	22.8	76	14	US-10-207-295-7	Sequence 7, Appl
18	83	20.1	67	9	US-09-756-854-26	Sequence 26, Appl
19	83	20.1	67	13	US-10-041-574-26	Sequence 26, Appl
20	83	20.1	67	16	US-10-834-966-26	Sequence 26, Appl
21	74	17.9	76	14	US-10-207-295-8	Sequence 8, Appl
22	70.5	17.1	77	13	US-10-112-793-27	Sequence 27, Appl
23	70.5	17.1	77	14	US-10-287-594-7	Sequence 7, Appl
24	68	16.5	67	9	US-09-756-854-25	Sequence 25, Appl
25	68	16.5	67	13	US-10-041-574-25	Sequence 25, Appl
26	68	16.5	67	16	US-10-834-966-25	Sequence 25, Appl
27	64.5	15.6	65	14	US-10-001-254-56	Sequence 56, Appl
28	63	15.3	62	15	US-10-424-599-188281	Sequence 188281,
29	60	14.5	77	17	US-10-656-250-118	Sequence 118, App
30	57.5	13.9	63	13	US-10-035-408-1	Sequence 1, Appl
31	57.5	13.9	68	9	US-09-756-854-22	Sequence 22, Appl
32	57.5	13.9	68	9	US-09-796-692-721	Sequence 721, App
33	57.5	13.9	68	13	US-10-041-574-22	Sequence 22, App
34	57.5	13.9	68	14	US-10-040-862-721	Sequence 721, App
35	57.5	13.9	68	15	US-10-057-4758-721	Sequence 721, App
36	57.5	13.9	68	15	US-10-354-884B-721	Sequence 721, App
37	57.5	13.9	68	16	US-10-764-324-721	Sequence 721, App
38	57.5	13.9	68	16	US-10-834-966-22	Sequence 22, App
39	57.5	13.9	77	9	US-09-887-879-17	Sequence 17, Appl
40	57.5	13.9	77	9	US-09-992-964-17	Sequence 17, Appl
41	57.5	13.9	77	13	US-10-112-793-24	Sequence 24, Appl
42	57.5	13.9	77	14	US-10-207-295-11	Sequence 11, Appl
43	57.5	13.9	77	14	US-10-242-383-17	Sequence 17, Appl
44	57	13.8	60	16	US-10-437-963-139854	Sequence 139854,
45	57	13.8	65	14	US-10-001-254-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1  
US-09-887-879-15  
; Sequence 15, Application US/09887879  
; Patent No. US20020102706A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chuntharapai, Anan  
; APPLICANT: Gurney, Austin  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Apo-2dcr  
; FILE REFERENCE: P1110P1  
; CURRENT APPLICATION NUMBER: US/09/887,879  
; CURRENT FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 09/096,500  
; PRIOR FILING DATE: 1998-06-12  
; PRIOR APPLICATION NUMBER: US 60/049,911  
; PRIOR FILING DATE: 1997-06-18  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 15  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-887-879-15

Query Match 92.3%; Score 381; DB 9; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.2e-38; Indels 0; Gaps 0;  
Matches 74; Conservative 0; Mismatches 0;

Qy 1 VMDAVPARRWKEFVRTIGLR...EAEVEVEIGRFRDQOQYEMLKRWROQOQAGLGAVYAAL 60

Db 1 VMDAVPARRWKEFVRTIGLR...EAEVEVEIGRFRDQOQYEMLKRWROQOQAGLGAVYAAL 60



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Qy 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 2
US-09-992-964-15
; Sequence 15, Application US/09992964
; Publication No. US20020161202A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: P110
; CURRENT APPLICATION NUMBER: US/09/992,964
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 08/878,168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-964-15

Query Match 92.3%; Score 381; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOYEMLKRWROOQPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOYEMLKRWROOQPAGLGAVYAAL 60

Qy 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 3
US-10-207-295-9
; Sequence 9, Application US/10207295
; Publication No. US20030017161A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung Jin
; TITLE OF INVENTION: APO-2 RECEPTOR
; FILE REFERENCE: 11669.28US04
; CURRENT APPLICATION NUMBER: US/10/207,295
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/09/020,746
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 08/857,216
; PRIOR FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-295-9

Query Match 92.3%; Score 381; DB 14; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOYEMLKRWROOQPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOYEMLKRWROOQPAGLGAVYAAL 60

Qy 61 ERMGLDGCVEDLRS 74
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Db 61 ERMGLDGCVEDLRS 74

RESULT 4
US-10-242-383-15
; Sequence 15, Application US/10242383
; Publication No. US20030138915A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: P110P1
; CURRENT APPLICATION NUMBER: US/10/242,383
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US/05/887,879
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-383-15

Query Match 92.3%; Score 381; DB 14; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOYEMLKRWROOQPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOYEMLKRWROOQPAGLGAVYAAL 60

Qy 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 5
US-09-756-854-24
; Sequence 24, Application US/09756854
; Patent No. US20020164684A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-756-854-24

Query Match      81.8%; Score 338; DB 9; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 60

Qy 69 VEDLR 73
|
Db 61 VEDLR 65

RESULT 6
US-10-041-574-24
; Sequence 24, Application US/10041574
; Publication No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/041,574
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-24

Query Match      81.8%; Score 338; DB 13; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 60

Qy 69 VEDLR 73
|
Db 61 VEDLR 65

RESULT 7
US-10-834-966-24
; Sequence 24, Application US/10834966
; Publication No. US20040197870A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/834,966
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US/10/041,574
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-834-966-24

Query Match      81.8%; Score 338; DB 16; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 60

Qy 69 VEDLR 73
|
Db 61 VEDLR 65

RESULT 8
US-09-887-879-16
; Sequence 16, Application US/09887879
; Patent No. US20020102706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P1110P1
; CURRENT APPLICATION NUMBER: US/09/887,879
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens

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; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-756-854-24

Query Match      81.8%; Score 338; DB 9; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 60

Qy 69 VEDLR 73
|
Db 61 VEDLR 65

RESULT 6
US-10-041-574-24
; Sequence 24, Application US/10041574
; Publication No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/041,574
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-24

Query Match      81.8%; Score 338; DB 13; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 60

Qy 69 VEDLR 73
|
Db 61 VEDLR 65

RESULT 7
US-10-834-966-24
; Sequence 24, Application US/10834966
; Publication No. US20040197870A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/834,966
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US/10/041,574
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-834-966-24

Query Match      81.8%; Score 338; DB 16; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVRLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 60

Qy 69 VEDLR 73
|
Db 61 VEDLR 65

RESULT 8
US-09-887-879-16
; Sequence 16, Application US/09887879
; Patent No. US20020102706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P1110P1
; CURRENT APPLICATION NUMBER: US/09/887,879
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens

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RESULT 12
US-10-242-383-16
; Sequence 16, Application US/10242383
; Publication No. US20030138915A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: Pl10P1
; CURRENT APPLICATION NUMBER: US/10/242,383
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US/09/887,879
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-383-16

Query Match      .    37.5%; Score 155; DB 14; Length 78;
Best Local Similarity 46.1%; Pred. No. Se-I1;
Matches   35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;

QY       1 VMDAPARRWKEFVRTGLREAEIYEVEIGR-FRDQQYEMLKRWQQQP---AGLCAV 56
        |::|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB       1 VVENVPPLRWKFEVRRGLSDHEIDRLQLNGRCLEAQYSMLATWRRTPRREATLELL 60
        ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:

QY       57 YAALERMGLDGCVEDL 72
        ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB       61 GRVLDRMDLLGCLEDI 76

RESULT 13
US-09-756-854-23
; Sequence 23, Application US/09756854
; Patent No. US20020164684A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
            Yu, Guo-Liang
            Fan, Ping
            Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
            ADDRESSEE: Human Genome Sciences, Inc.
            STREET: 9410 Key West Avenue
            CITY: Rockville
            STATE: MD
            COUNTRY: US
            ZIP: 20850
; COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/756,854
            FILING DATE: 10-Jan-2001
            CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 09/095,094
            FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
            NAME: Hoover, Kenley K.
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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:32:34 ; Search time 43 seconds  
(without alignments)  
138.882 Million cell updates/sec

Title: US-10-081-280-6\_COPY\_338\_417

Perfect score: 413

Sequence: 1 VMDAVPARRWKEFVRLTLGLR.....ERMGLDGCVDLRSLRQGP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 307244

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338	81.8	65	3	US-09-527-236A-24
2	338	81.8	65	4	US-09-756-854-24
3	155	37.5	78	4	US-08-828-683A-23
4	142	34.4	70	4	US-09-159-277A-6
5	142	34.4	70	4	US-08-844-691A-6
6	136.5	33.1	68	3	US-09-527-236A-23
7	136.5	33.1	68	4	US-09-756-854-23
8	118	28.6	64	3	US-08-894-626-3
9	102.5	24.8	45	2	US-08-219-237B-11
10	83	20.1	67	3	US-09-527-236A-26
11	83	20.1	67	4	US-09-756-854-26
12	73.5	17.8	41	1	US-08-444-005-28
13	70.5	17.1	77	3	US-08-995-159-7
14	70.5	17.1	77	4	US-08-828-683A-27
15	70.5	17.1	77	4	US-09-545-605-7
16	68	16.5	40	1	US-08-444-005-22
17	68	16.5	67	3	US-09-527-236A-25
18	68	16.5	67	4	US-09-756-854-25
19	67	16.2	41	1	US-08-444-005-23
20	67	16.2	51	3	US-08-883-036A-4
21	67	16.2	51	4	US-09-536-201-4
22	67	16.2	51	4	US-09-578-392-4
23	65.5	15.9	41	1	US-08-444-005-29
24	60	14.5	77	4	US-09-069-827A-118
25	59	14.3	68	3	US-08-995-050-1
26	57.5	13.9	45	2	US-08-219-237B-10
27	57.5	13.9	63	3	US-08-894-626-1

28	57.5	13.9	68	3	US-09-527-236A-22	Sequence 22, Appl
29	57.5	13.9	68	4	US-09-756-854-22	Sequence 22, Appl
30	57.5	13.9	70	4	US-09-159-277A-5	Sequence 5, Appl
31	57.5	13.9	70	4	US-08-844-691A-5	Sequence 5, Appl
32	57.5	13.9	77	4	US-08-828-683A-24	Sequence 24, Appl
33	54.5	13.2	63	3	US-08-894-626-2	Sequence 2, Appl
34	54	13.1	25	2	US-08-580-988A-27	Sequence 27, Appl
35	54	13.1	56	3	US-08-894-626-4	Sequence 4, Appl
36	50.5	12.2	74	3	US-09-134-001C-5122	Sequence 5122, Ap
37	50	12.1	37	4	US-09-653-465B-6	Sequence 6, Appl
38	50	12.1	67	3	US-09-527-236A-21	Sequence 21, Appl
39	50	12.1	67	4	US-09-756-854-21	Sequence 21, Appl
40	49	11.9	67	4	US-09-902-540-10142	Sequence 10142, A
41	49	11.9	68	3	US-09-134-001C-3076	Sequence 3076, Ap
42	49	11.9	68	3	US-09-134-001C-3335	Sequence 3335, Ap
43	49	11.9	68	3	US-09-134-001C-3730	Sequence 3730, Ap
44	49	11.9	68	3	US-09-134-001C-3898	Sequence 3898, Ap
45	49	11.9	68	3	US-09-134-001C-4232	Sequence 4232, Ap

ALIGNMENTS

RESULT 1  
US-09-527-236A-24  
; Sequence 22, Appl  
; Patent No. 6358508  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Fan, Ping  
; APPLICANT: Gentz, Reiner L.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
; FILE REFERENCE: PF375P1  
; CURRENT APPLICATION NUMBER: US/09/527,236A  
; CURRENT FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/052,991  
; PRIOR FILING DATE: 1997-06-11  
; PRIOR APPLICATION NUMBER: 09/095,094  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/126,019  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: 60/134,220  
; PRIOR FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-527-236A-24

Query Match 81.8%; Score 338; DB 3; Length 65;  
Best Local Similarity 100.0%; Pred. No. 6.2e-37; Indels 0; Gaps 0;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 RWKEFVRLTLGLREAEI EAVEVEIGRFRDQQYEMLKRWQQQPAGLGAVYAALERMGLDGC 68  
DB 1 RWKEFVRLTLGLREAEI EAVEVEIGRFRDQQYEMLKRWQQQPAGLGAVYAALERMGLDGC 60  
QY 69 VEDLR 73  
DB 61 VEDLR 65

RESULT 2  
US-09-756-854-24  
; Sequence 24, Appl  
; Patent No. 6667390  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Fan, Ping



TELEFAX: (650)494-0792  
TELEX: 706141 MRSNFOERS SFO  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 70 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: /note= "Leu is replaced by Asn for  
OTHER INFORMATION: the point mutant hTNR-1"  
US-09-159-277A-6

Query Match 34.4%; Score 142; DB 4; Length 70;  
Best Local Similarity 47.1%; Pred. No. 3.4e-11;  
Matches 32; Conservative 11; Mismatches 21; Indels 4; Gaps 2;

QY 9 RWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWRRQQP---AGLGAVYAALERMG 64  
Db 1 RWKEFVRLGLSDHEIDRLQNGRCLEAQYSLATWRRTPREATLELLGRVLRDMD 60

QY 65 LDGCVEDL 72  
Db 61 LIGCLEDI 68

RESULT 5  
US-08-844-691A-6  
Sequence 6, Application US/08844691A  
Patent No. 6747138  
GENERAL INFORMATION:  
APPLICANT: DIXIT, VISHVA M.  
APPLICANT: O'ROURKE, KAREN  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING  
TITLE OF INVENTION: FAS-ASSOCIATED APOPTOSIS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/844,691A  
FILING DATE: 21-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/416,379  
FILING DATE: 03-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Koneki, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442107001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)813-5600  
TELEFAX: (650)494-0792  
TELEX: 706141 MRSNFOERS SFO  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 70 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: /note= "Leu is replaced by Asn for  
OTHER INFORMATION: the point mutant hTNR-1"  
US-08-844-691A-6

Query Match 34.4%; Score 142; DB 4; Length 70;  
Best Local Similarity 47.1%; Pred. No. 3.4e-11;  
Matches 32; Conservative 11; Mismatches 21; Indels 4; Gaps 2;

QY 9 RWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWRRQQP---AGLGAVYAALERMG 64  
Db 1 RWKEFVRLGLSDHEIDRLQNGRCLEAQYSLATWRRTPREATLELLGRVLRDMD 60

QY 65 LDGCVEDL 72  
Db 61 LIGCLEDI 68

RESULT 6  
US-09-527-236A-23  
Sequence 23, Application US/09527236A  
Patent No. 6358508  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Fan, Ping  
APPLICANT: Gentz, Reiner L.  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
FILE REFERENCE: PF375P1  
CURRENT APPLICATION NUMBER: US/09/527,236A  
CURRENT FILING DATE: 2000-03-16  
PRIOR APPLICATION NUMBER: 60/052,991  
PRIOR FILING DATE: 1997-06-11  
PRIOR APPLICATION NUMBER: 09/095,094  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/126,019  
PRIOR FILING DATE: 1999-03-24  
PRIOR APPLICATION NUMBER: 60/134,220  
PRIOR FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 23  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-527-236A-23

Query Match 33.1%; Score 136.5; DB 3; Length 68;  
Best Local Similarity 46.3%; Pred. No. 1.7e-10;  
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

QY 9 RWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWRRQQP---AGLGAVYAALERMGL 65  
Db 1 RWKEFVRLGLSDHEIDRLQNGRCLEAQYSLATWRRTPREATLELLGRVLRDMDL 60

QY 66 DGCVEDL 72  
Db 61 LIGCLEDI 67

RESULT 7  
US-09-756-854-23  
Sequence 23, Application US/09756854  
Patent No. 6667390  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Fan, Ping  
APPLICANT: Gentz, Reiner  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
NUMBER OF SEQUENCES: 26



; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/756,854  
; FILING DATE: 10-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/095,094  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoover, Kenley K.  
; REGISTRATION NUMBER: 40,302  
; REFERENCE/DOCKET NUMBER: PF375  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 68 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-756-854-23  
  
Query Match 33.1%; Score 136.5; DB 4; Length 68;  
Best Local Similarity 46.3%; Pred. No. 1.7e-10;  
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;  
  
Qy 9 RWKEFVRTLGREAEIEAVEVEIGR-FRDOQYEMLKRWQ--QQPAGLGAVYAALERMGL 65  
Db 1 RWKEFVRLGLSDHIDRLQLNGRCLEAQYSMLATWRRRTREATLLGLRVLRDMDL 60  
  
Qy 66 DGCVEDL 72  
Db 61 LGCLEDI 67  
  
RESULT 8  
US-08-894-626-3  
; Sequence 3, Application US/08894626  
; Patent No. 6355780  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; BOLDIN, Mark P.  
; VARFOLOMEEV, Eugene E.  
; PANCER, Zeev  
; METT, Igor  
; GONCHAROV, Tanya M.  
; WEINWURZEL, Henry  
; TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/894,626  
; FILING DATE: 09-Dec-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 112,742  
; FILING DATE: 22-FEB-1995  
; APPLICATION NUMBER: IL 115,289  
; FILING DATE: 13-SEP-1995  
; APPLICATION NUMBER: PCT/US96/02326  
; FILING DATE: 15-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH=17  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 64 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-894-626-3  
  
Query Match 28.6%; Score 118; DB 3; Length 64;  
Best Local Similarity 42.6%; Pred. No. 4.3e-08;  
Matches 29; Conservative 10; Mismatches 17; Indels 12; Gaps 3;  
  
Qy 10 WKKEFVRTLGREAEIEAVEVEIGR-FRDOQYEMLKRWQOQPAGLGAVYAALERMG---- 64  
Db 1 WKKEFVRLGLSDHIDRLQLNGRCLEAQYSMLATWRRRTPRR-----EATLELLGRVLR 56  
  
Qy 65 ---LDGCV 69  
Db 57 DHDLGLCL 64  
  
RESULT 9  
US-08-219-237B-11  
; Sequence 11, Application US/08219237B  
; Patent No. 5874546  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu  
; APPLICANT: ITOH, Naoto  
; APPLICANT: YONEHARA, Shin  
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James W. Hellwege  
; STREET: P.O. Box 2266 Eads Station  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/219,237B  
; FILING DATE: 28-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/872,129  
; FILING DATE: 22-APR-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

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; NAME: James W. Hellwege
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 516762
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-219-237B-11

Query Match 24.8%; Score 102.5; DB 2; Length 45;
Best Local Similarity 51.2%; Pred. No. 2.9e-06;
Matches 21; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

Qy 11 KEFVRTGLGREAEVEIGR-FRDOQYEMLKRWQQQP 50
Db 1 KEFVRTGLSDHEIDRLBLQNGRCLEAQYSLATWRRTP 41

RESULT 10
US-09-527-236A-26
; Sequence 26, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 26
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-26

Query Match 20.1%; Score 83; DB 3; Length 67;
Best Local Similarity 33.3%; Pred. No. 0.0018;
Matches 19; Conservative 11; Mismatches 25; Indels 2; Gaps 1;

Qy 10 WKEFVRTGLGREAEVEIGRFRDOQYEMLKRW--RQQPAGLGAVYAALRMG 64
Db 2 WEPLMRKLGMDNEIKVAKAEAGHRDRLTYTMLIKWVNTGRDASVHTLLDALETG 58

RESULT 11
US-09-756-854-26
; Sequence 26, Application US/09756854
; Patent No. 6667390
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
```

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; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-756-854-26

Query Match 20.1%; Score 83; DB 4; Length 67;
Best Local Similarity 33.3%; Pred. No. 0.0018;
Matches 19; Conservative 11; Mismatches 25; Indels 2; Gaps 1;

Qy 10 WKEFVRTGLGREAEVEIGRFRDOQYEMLKRW--RQQPAGLGAVYAALRMG 64
Db 2 WEPLMRKLGMDNEIKVAKAEAGHRDRLTYTMLIKWVNTGRDASVHTLLDALETG 58

RESULT 12
US-08-444-005-28
; Sequence 28, Application US/08444005
; Patent No. 5674734
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Seed, Brian
; APPLICANT: Stanger, Ben Z.
; APPLICANT: Lee, Tae-Ho
; APPLICANT: Kim, Emily
; TITLE OF INVENTION: CELL DEATH PROTEIN
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,005
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,164
; REFERENCE/DOCKET NUMBER: 00383/026001
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